

DR N-PSDB; ABK83232.

XX New high growth methanotrophic bacterial strain, useful for producing
 ET single cell proteins, grows on a C1 carbon substrate, and comprises a
 PT functional gene encoding in Embden-Meyerhof carbon pathway

PS Claim 7; Page 85-87; 157pp; English.

XX The invention relates to a high growth methanotrophic bacterial strain,
 CC which grows on a C1 carbon substrate e.g. methane and methanol, and
 CC comprises a functional Embden-Meyerhof carbon flux pathway comprising a
 CC gene coding a pyrophosphate dependent phosphotrikinase enzyme or a 16s
 CC RNA. The bacterial strain is useful for the production of single cell
 CC protein and for the biotransformation of a nitrogen-containing compound,
 CC e.g. ammonia, nitrate, nitrite or nitrogen. It is also useful for the
 CC production of a feed product comprising a protein, carbohydrates and a
 CC pigment and for reducing oxygen demand, for removing nitrates and
 CC nitrates in methane-containing environments such as landfills, waste
 CC water treatment systems or anywhere that methane, oxygen and nitrates are
 CC present. The bacterial strain of the invention can be used as a
 CC denitrifying agent for the conversion of nitrate or nitrite to nitrous
 CC oxide with methane or methanol as a carbon source. It is also used in the
 CC production of biomass including proteins, carbohydrates and a wide
 CC variety of pigments (particularly for isoprenoid pigments for the
 CC purpose of generating animal feeds), in production of terpenoid and
 CC carotenoid compounds, useful as pigments and as monomers in polymeric
 CC materials and in production of exopolysaccharides at high levels.
 CC Sequences ABG61551-ABG61590 represent high growth methanotrophic
 CC bacterial strain proteins of the invention.

XX Sequence 437 AA;

Query Match 100.0%; Score 2284; DB 23; Length 437;

Best Local Similarity 100.0%; Pred. No. 2e-207;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTWTPYHLTADIRFCGMFFNFNTLMNKPKKVAIITAGGLAPCLNSAIGLIERYTE 60
 DB 1 DVTWTPYHLTADIRFCGMFFNFNTLMNKPKKVAIITAGGLAPCLNSAIGLIERYTE 60
 QY 61 IDPSIEIICYRGYKGLLGDSPVTAVERKKAGVLOFGGSVIGNSRVKLTNVKDCVCR 120
 DB 61 IDPSIEIICYRGYKGLLGDSPVTAVERKKAGVLOFGGSVIGNSRVKLTNVKDCVCR 120
 QY 121 GLVKEGDDPOKVAADQVLDGVDILHTIGDDDTNTAAADLAAPLARNNGELTVIGPKTV 180
 DB 121 GLVKEGDDPOKVAADQVLDGVDILHTIGDDDTNTAAADLAAPLARNNGELTVIGPKTV 180
 QY 121 GLVKEGDDPOKVAADQVLDGVDILHTIGDDDTNTAAADLAAPLARNNGELTVIGPKTV 180
 DB 121 GLVKEGDDPOKVAADQVLDGVDILHTIGDDDTNTAAADLAAPLARNNGELTVIGPKTV 180
 QY 181 DNDVFPFKOSLIGAWTAAGARFYFNVAENANPRLIVHEWGRNCGMLTAATQOEYR 240
 DB 181 DNDVFPFKOSLIGAWTAAGARFYFNVAENANPRLIVHEWGRNCGMLTAATQOEYR 240
 QY 241 KLDDRAEWLPELGLTRSEYEVHNVFVPMALDLEAEKLELVNDKRDVCNITPSEBAGY 300
 DB 241 KLDDRAEWLPELGLTRSEYEVHNVFVPMALDLEAEKLELVNDKRDVCNITPSEBAGY 300
 QY 301 EAIYVEMAKOQOEVRDPAFGHILKDAVPMKMFQGFQOMIGAKETLVOKSGYFARASAS 360
 DB 301 EAIYVEMAKOQOEVRDPAFGHILKDAVPMKMFQGFQOMIGAKETLVOKSGYFARASAS 360
 QY 361 NVDDMRILKSCADLAVECAFRESGVIGHDEEDNGNVLPAIEFPRIKGGKFNITDWPNS 420
 DB 361 NVDDMRILKSCADLAVECAFRESGVIGHDEEDNGNVLPAIEFPRIKGGKFNITDWPNS 420
 QY 421 MLSEIIGQPKGKGVESH 437
 DB 421 MLSEIIGQPKGKGVESH 437

RESULT 2
 AAE22299
 ID AAE22299 standard; Protein; 437 AA.

AC AAE22299;

XX 25-JUL-2002 (first entry)

DE Methylomonas 16a sp. phosphotrikinase pyrophosphate dependent enzyme.

KM Carotenoid; isopentenyl pyrophosphate; anthraxanthin; astaxanthin; diet;

KM anti-oxidant; steroid; fragrance; electro-optic application;

XX aquaculture; enzyme; phosphotrikinase pyrophosphate.

OS Methylomonas 16a sp.

PM WC200218617-A2.

PD 07-MAR-2002.

PF 04-SEP-2001; 2001MO-US27420.

PR 01-SEP-2000; 2000US-229858P.

PR 01-SEP-2000; 2000US-229907P.

PA (DUPO) DU PONT DE NEMOURS & CO E. I.

PI Brzostowicz PC, Cheng Q, Dicosimo DJ, Koffas M, Miller ES;

PI Odum JM, Picataggio SK, Rouviere PB;

DR WPI; 2002-351711/38.

XX N-PSDB; AAD35497.

XX Producing carotenoid compounds e.g. anthraxanthin and astaxanthin, by

PT using microorganisms having a nucleic acid molecule encoding enzymes in

PT the carotenoid biosynthetic pathway and which metabolize single carbon

PT substrates

PS Claim 8; Page 104-106; 156pp; English.

XX The invention relates to a method for producing carotenoid compounds.

CC The method comprises a transformed metabolising host cell, comprising

CC suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule

CC encoding an enzyme in the carotenoid biosynthetic pathway, under the

CC control of regulatory sequences, and contacting the host cell with carbon

CC substrate to produce a carotenoid compound. The method is useful for

CC producing carotenoid compounds such as anthraxanthin and astaxanthin, by

CC using microorganisms having a nucleic acid molecule encoding enzymes in

CC the carotenoid biosynthetic pathway and which metabolize single carbon

CC substrates. The carotenoids have potent anti-oxidant properties useful in

CC diet, and aquaculture elements. The carotenoids are also useful as

CC intermediates in the synthesis of steroids flavours and fragrances and

CC compounds for potential electro-optic applications. The present sequence

CC is Methylomonas 16a sp. phosphotrikinase pyrophosphate dependent

CC enzyme used in the invention.

XX Sequence 437 AA;

Query Match 100.0%; Score 2284; DB 23; Length 437;

Best Local Similarity 100.0%; Pred. No. 2e-207;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTWTPYHLTADIRFCGMFFNFNTLMNKPKKVAIITAGGLAPCLNSAIGLIERYTE 60
 DB 1 DVTWTPYHLTADIRFCGMFFNFNTLMNKPKKVAIITAGGLAPCLNSAIGLIERYTE 60
 QY 61 IDPSIEIICYRGYKGLLGDSPVTAVERKKAGVLOFGGSVIGNSRVKLTNVKDCVCR 120
 DB 61 IDPSIEIICYRGYKGLLGDSPVTAVERKKAGVLOFGGSVIGNSRVKLTNVKDCVCR 120
 QY 121 GLVKEGDDPOKVAADQVLDGVDILHTIGDDDTNTAAADLAAPLARNNGELTVIGPKTV 180
 DB 121 GLVKEGDDPOKVAADQVLDGVDILHTIGDDDTNTAAADLAAPLARNNGELTVIGPKTV 180
 QY 181 DNDVFPFKOSLIGAWTAAGARFYFNVAENANPRLIVHEWGRNCGMLTAATQOEYR 240
 DB 181 DNDVFPFKOSLIGAWTAAGARFYFNVAENANPRLIVHEWGRNCGMLTAATQOEYR 240

QY 241 KILDRAEWLPGLTRESYEVHAFVPEMAIDLEAKRLREVMKVDVCNIFVSEGAGV 300
 DB 241 KILDRAEWLPGLTRESYEVHAFVPEMAIDLEAKRLREVMKVDVCNIFVSEGAGV 300
 QY 301 EAIIVAMOKAGOEVRPDAGHITKLDVNPGRKFGSGOPAMIGAKETLVOKSGYFARASAS 360
 DB 301 EAIIVAMOKAGOEVRPDAGHITKLDVNPGRKFGSGOPAMIGAKETLVOKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRRBSGVIGHDEDNQNVLAIEFPRIKGGKPFNIDTDFNS 420
 DB 361 NVDDMRLLKSCADLAVECAFRRBSGVIGHDEDNQNVLAIEFPRIKGGKPFNIDTDFNS 420
 QY 421 MLSEIGQPKGKVEVSH 437
 DB 421 MLSEIGQPKGKVEVSH 437
 RESULT 3
 ABB09168 standard; Protein; 437 AA.
 ID ABB09168;
 AC ABB09168;
 XX
 DT 01-JUL-2002 (first entry)
 DE Methylomonas pyrophosphate dependent phosphofructokinase SEQ ID NO.16.
 XX
 KM Methylomonas; methanotropic; carbon metabolism; carbon flux pathway;
 KM transaldolase; fructose biphosphate aldolase; KMG/KDPG aldolase; food;
 KM pyrophosphate dependent phosphofructokinase; phosphoglucumutase; feed;
 KM glucose 6 phosphate isomerase; 6-phosphogluconate dehydratase; methane;
 KM glucose 6 phosphate 1 dehydrogenase; enzyme; methanotroph; methanol;
 KM single carbon substrate; single cell protein; polysaccharide; thickener;
 KM isoprenoid; carotenoid pigment.
 XX
 OS Methylomonas sp.
 XX
 FM WO200220796-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 28-AUG-2001; 2001WO-US26730.
 XX
 PR 01-SEP-2000; 2000US-229906P.
 XX
 PA (DUPO) DU POINT DE MEMOIRS & CO E I.
 PI Koffas M, Odem JM, Norton KC, Ye RW;
 DR MPI: 2002-362250/39.
 XX
 DR N-PSDB; ABJ51513.
 XX
 PT New polynucleotide encoding a Methylomonas sp. carbon flux enzyme
 PT useful for altering carbon flow through methanotrophic bacteria,
 PT utilized for production of single cell protein and commercially
 PT valuable polysaccharides -
 XX
 PS Claim 4; Page 66-68; 73pp; English.
 XX
 CC The present invention describes isolated polynucleotides (I) encoding a
 CC Methylomonas sp. carbon flux enzyme, consisting of: transaldolase;
 CC fructose biphosphate aldolase; KMG/KDPG aldolase; phosphoglucumutase;
 CC pyrophosphate dependent phosphofructokinase; glucose 6 phosphate
 CC isomerase; 6-phosphogluconate dehydratase; and glucose 6 phosphate 1
 CC dehydrogenase enzymes. (i) overexpression is useful for altering carbon
 CC flow through a methanotrophic bacteria, where the bacteria grows on a C1
 CC carbon substrate of methane and methanol, and comprises a functional
 CC Embden-Meyerhof carbon pathway comprising a gene encoding a pyrophosphate
 CC dependent phosphofructokinase enzyme, where the bacteria is preferably
 CC Methylomonas 16a American Type Culture Collection (ATCC) PTA 2402, and
 CC where the carbon flux gene is: (i) over-expressed on a multicopy plasmid;
 CC (ii) operably linked to an inducible or regulated promoter;

CC (iii) expressed in an antisense orientation, or (iv) disrupted by
 CC insertion of foreign DNA into the coding region. The manipulated
 CC methanotrophs are useful for the energy efficient conversion of single
 CC carbon substrates such as methane and methanol to commercially useful
 CC products in the food, feed and materials industries, and preferably for
 CC the production of single cell protein, and for producing polysaccharides,
 CC used as thickeners in food and non-food industries, and isoprenoid
 CC compounds and carotenoid pigments of various carbon lengths. The present
 CC sequence represents a Methylomonas pyrophosphate dependent
 CC phosphofructokinase from the present invention.
 XX
 SQ Sequence 437 AA;
 Query Match 100.0%; Score 2284; DB 23; Length 437;
 Best Local Similarity 100.0%; Pred. No. 2e-207;
 Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVVTMPYHLTADIFGCHWFILNFPTLMNPKKVAITTAGGLAPCLNSAIGSLIERTYE 60
 DB 1 DVVTMPYHLTADIFGCHWFILNFPTLMNPKKVAITTAGGLAPCLNSAIGSLIERTYE 60
 QY 61 IDPSIEIICYRGYKGLLDGSDYPVLAVERKAGVLRFGSGVIGNSRVKLTNNVDCVYR 120
 DB 61 IDPSIEIICYRGYKGLLDGSDYPVLAVERKAGVLRFGSGVIGNSRVKLTNNVDCVYR 120
 QY 121 GLVKEGEDPQRYAADOLVKOGVDILHTIGSDDTYTAADLAFLARNYGLTVIGLPTTV 180
 DB 121 GLVKEGEDPQRYAADOLVKOGVDILHTIGSDDTYTAADLAFLARNYGLTVIGLPTTV 180
 QY 181 DNDVFPFQSGIAGTAAFGARYFNVAENNAFPMILIVHEVGRNCGMTLTAATAGERYR 240
 DB 181 DNDVFPFQSGIAGTAAFGARYFNVAENNAFPMILIVHEVGRNCGMTLTAATAGERYR 240
 QY 241 KILDRAEWLPGLTRESYEVHAFVPEMAIDLEAKRLREVMKVDVCNIFVSEGAGV 300
 DB 241 KILDRAEWLPGLTRESYEVHAFVPEMAIDLEAKRLREVMKVDVCNIFVSEGAGV 300
 QY 301 EAIIVAMOKAGOEVRPDAGHITKLDVNPGRKFGSGOPAMIGAKETLVOKSGYFARASAS 360
 DB 301 EAIIVAMOKAGOEVRPDAGHITKLDVNPGRKFGSGOPAMIGAKETLVOKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRRBSGVIGHDEDNQNVLAIEFPRIKGGKPFNIDTDFNS 420
 DB 361 NVDDMRLLKSCADLAVECAFRRBSGVIGHDEDNQNVLAIEFPRIKGGKPFNIDTDFNS 420
 QY 421 MLSEIGQPKGKVEVSH 437
 DB 421 MLSEIGQPKGKVEVSH 437
 RESULT 4
 AAU45865 standard; Protein; 410 AA.
 ID AAU45865;
 AC AAU45865;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #6761.
 XX
 KM SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KM uveitis; endophthalmitis; bone; joint; central nervous system; EUSA;
 KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KM dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 FM WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX

21-APR-2000; 2000US-199047P.
 02-JUN-2000; 2000US-208841P.
 07-JUL-2000; 2000US-216747P.
 (CORI-) CORIXA CORP.

Skelly YAM, Paring DH, Mitcham JL, Wang SS, Bhatia A;
 L'maisonmeuve J, Zhang Y, Jen S, Carter D;
 MPI; 2001-616774/71.
 N-PSDB; AAS59528.

Propionibacterium acnes polypeptides and nucleic acids useful for
 vaccinating against and diagnosing infections, especially useful for
 treating acne vulgaris -

Example 1; SEQ ID NO 7060; 1069pp; English.

Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic
 polypeptides. The proteins and their associated DNA sequences are used in
 the treatment, prevention and diagnosis of medical conditions caused by
 P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 P. acnes is also involved in infections of bone, joints and the central
 nervous system, however it is particularly involved in the inflammatory
 lesions associated with acne vulgaris. A method for detecting the
 presence or absence of P. acnes in a patient comprises contacting a
 sample with a binding agent that binds to the proteins of the invention
 and determining the amount of bound protein in the sample. The
 polypeptides may be used as antigens in the production of antibodies
 specific for P. acnes proteins. These antibodies can be used to
 downregulate expression and activity of P. acnes polypeptides and
 therefore treat P. acnes infections. The antibodies may also be used as
 diagnostic agents for determining P. acnes presence, for example, by
 enzyme linked immunosorbent assay (ELISA).
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 410 AA;

Query Match 63.1%; Score 1442; DB 22; Length 410;

Best Local Similarity 68.6%; Pred. No. 1e-127;

Matches 271; Conservative 54; Mismatches 70; Indels 0; Gaps 0;

33 KKVAILTAGGLAPCNSAIGSLIERYTEIDPSIEIICRGQYKGLGDSYPTAVYRKR 92
 15 KKVAILTAGGLAPCNSAIGSLIERYTEIDPSIEIICRGQYKGLGDSYPTAVYRKR 74
 93 AGVLQRFQGSVIGNSRVKLTNVKDCVVRGLVKEGEDPQKVAADQLVXGVDIILHTIGDD 152
 75 AEILIKREGSGSPIGNSRVKLTNVKDCVVRGLVKEGEDPQKVAADQLVXGVDIILHTIGDD 134
 153 TTTTAAADLAALANNNGLTIVIGLPTVNDVPPFIKOSLGAWTAAGQAYFMMVAVEN 212
 135 TTTTAAADLAALANNNGLTIVIGLPTVNDVPPFIKOSLGAWTAAGQAYFMMVAVEN 194
 213 ANPEMLIVHEVWGNCGMLTAATAOBYRKLDBRAEMLPELGLTRSEYVAVPEVAID 272
 195 SGGSLILYHEVWGNCGMLTAATAOBYRKLDBRAEMLPELGLTRSEYVAVPEVAID 254
 273 LEAAKRLREVMKDCVNTIVSFGAGYEAIVAEKQAGQEVPPDAAGHKLDAVNGK 332
 255 LEAAKRLREVMKDCVNTIVSFGAGYEAIVAEKQAGQEVPPDAAGHKLDAVNGK 314
 333 FGEFOAQMIGAEKTLVQKSGYFARASASNDVMDLIRKSCADLAVECAFRESGYLGHD 392
 315 FGEFOAQMIGAEKTLVQKSGYFARASASNDVMDLIRKSCADLAVECAFRESGYLGHD 374
 393 NGNVLAIRBPRIRKSGYFARASASNDVMDLIRKSCADLAVECAFRESGYLGHD 427
 375 NGNVLAIRBPRIRKSGYFARASASNDVMDLIRKSCADLAVECAFRESGYLGHD 409

RESULT 5
 ABB93840
 ID ABB93840 standard; Protein; 488 AA.
 XX

ABB93840;

31-MAY-2002 (first entry)

Herbicide; active polypeptide SEQ ID NO 3051.

Herbicide; plant; agriculture; herbicide.

Arabidopsis thaliana.

WO200210210-A2.

07-FEB-2002.

28-AUG-2001; 2001WO-EP09892.

28-AUG-2001; 2001WO-EP09892.

(PARB) BAYER AG.

Tietjen K, Weidler M;

WPI; 2002-269010/31.

Identifying plant target proteins for herbicidally active compounds,
 comprising aligning and comparing nucleic acid or amino acid sequences
 from plant with nucleic acid or amino acid sequences from non-plant
 organisms -

Claim 5; SEQ ID NO 3051; 261pp + Sequence listing; English.

The invention relates to identifying target proteins

(ABB90790-ABB94016) for herbicidally active compounds, comprising

aligning and comparing nucleic acid or amino acid sequences from plant

with nucleic acid or amino acid sequences from non-plant organisms using

suitable search parameters, where plant sequences having an E-value

greater by a factor of 3 than the E-value of most similar non-plant

sequences are selected. The polypeptides or nucleic acids encoding them

are useful for identifying the identified modulators. The identified modulators are

useful as herbicides.

SO Sequence 488 AA;

Query Match 12.3%; Score 282; DB 23; Length 488;

Best Local Similarity 26.8%; Pred. No. 1e-17;

Matches 112; Conservative 60; Mismatches 158; Indels 88; Gaps 18;

37 ILTAGGLAPCNSAIGSLIERYTEIDPSIEIICRGQYKGLGDSYPTAVYRKR 87
 96 IYCGGLCPGLNTVIREVSSLSYMGVRIIGIDVSL-----GGYRFYAKNTIPPLMS 149
 88 EYRKAGVLRQFGSVIGNSRVKLTNVKDCVVRGLVKEGEDPQKVAADQLVXGVDIILHT 147
 150 KY---VNDIHKRGGLTIGTSR-----GGHDTNKI-VDSIQRGINQVYI 189
 148 IGGDDTTAAADLAALANNNGLTIVIGLPTVNDVPPFIKOSLGAWTAAGQAYF--M 205
 190 IGGDDTQAGASVIFEEIRRRRLKAVAVGLPKTIIDNDIPITDSFGPDIVAEAGRAINA 249
 206 NYVAENANPEMLIVHEVWGNCGMLTAATAOBYRKLDBRAEMLPELGLTRSEYVAV 265
 250 HYAEASNNENIGFV---KLMGRYSYIA-----MYATLASRDVDCCL 288
 266 VPEMAIDLEAA-----KRLREVMKDCVNTIVSFGAGYEAIVAEKQAGQEVPPDA 318
 289 IPSPFYLEGSGGLFEFFIRRLKDHGHW---IYABAGQDLCKSKES---TPMDA 340
 319 FGHIKLDVAVNPKMGGEOPQAMIGAEKTLVQ---KSGYFARASASNDVMDLIRKSCADL 374

Db 341 SGRKLEKDV--GLMISQSIKDHFKNNKRWMTKYIDPTMIRAVPNSADNVYCTLLAQS 398
QY 375 AVECAFRRESGVIGHDED--NENVLRAIFEPRIKSGKEPNIDTD--WENSMLEIGQP 428
Db 399 AVHGAM--AGTGTGYSGLVNER-QTYIFVYRITERQNNVYITDRMMAR-LISSTNQP 451

RESULT 6
AAG39480
ID AAG39480 standard; Protein; 485 AA.
XX
AC AAG39480;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SBQ ID NO: 48654.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-01332407.
PR 05-MAY-1999; 99US-01332484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142802.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156556.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158222.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 12.3%; Score 281.5; DB 21; Length 485;
Best Local Similarity 26.7%; Pred. No. 1,1e-17;
Matches 109; Conservative 61; Mismatches 166; Indels 73; Gaps 16;
QY 37 ILTGGLAPCNSMIGSIRYETIDPSISIFICRGYKGLLDSPYTAERKAGV. 96
DB 96 IVTGGGICPGNTVIREVSSLSYMGVGRILGIDGREGYAKNTPLNSKV---VNDI 152

QY 97 QRFQSVIAGNSRKYLTNNKDCYKGLVKEGEDPQKVAADQLYKQGVDIHTIGSDPTNFA 156
DB 153 HRRGGTIIIGTSR-----GGHTNNI-VDSIODRGINOVYIIIGSGGTORG 195
QY 157 AADLAFLARNNYGLTVIGLPTVNDVPEIKOSIGAWTAEOGARVF--NNVVAENNAY 214
DB 196 ASVIFEEIRRLKRAVAVGIPKTIINDIPIVDKSGPDIABEAGRAIIPAAVEAESNEN 255
QY 215 PMLIVHEVNGNCGMLTPATAGSEYKLLDRAMLPZGLTSESYVAVAFPEPAIDIE 274
DB 256 GIGFV--KLNGRYSGVIA-----WATLASADVDCLLPESEFYIE 294
QY 275 AEA-----KLRPMQKVDGCVNIFVSEGAQVEAIVEMQKQVEPRDAIGHIKLDAY 327
DB 295 GEGGLPEPIERKLRKHGMV-----IVLAGAGQDLCKMSBES---TPMDASGNKLDKV 346
QY 328 NKGKWPGEQPAQMGAEKTLVQ---KSGYPARASAVNDRLIKSCADLAVECAFRRE 383
DB 347 --GLMWSQSIKDHFKKMKVMMLAKYIDFTYMIKRAVPSNADRVYCTLLAQSAVHGAM--- 401
QY 384 SGVIGHDED--NGNVLRAIEFPRKIGKGFNDTP--NFNSMLSEIGOP 428
DB 402 AGTGTSGLVNGR-QTYIPFRTITETONNVITDRPMAR-LDSSTNOF 448
RESULT 7
AAR71580
ID AAR71580 standard; Protein; 483 AA.
XX AAR71580;
AC
XX 25-MAR-2003 (updated)
DT 11-OCT-1995 (first entry)
XX
DE Flavaria brownii fructose-6-phosphate 1-phosphotransferase.
XX
KW ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme; plant;
KW potato; Solanum tuberosum; rice; Oryza sativa; maize; Zea mays; radish;
KW Raphanus sativus; Flavaria brownii; primer; expression vector;
XX Agrobacterium tumefaciens; sugar; storage; temperature.
XX
OS Flavaria brownii.
XX
XX
PN W09505457-A1.
XX
XX 23-FEB-1995.
PD
XX
PF 16-AUG-1994; 94WO-JP01352.
XX
XX 19-AUG-1993; 93JP-0226454.
PR
XX (NISR) JAPAN TOBACCO INC.
PA
XX
XX Hiyoshi T, Kaseoka K, Mine T, Page MJ, Tyson HR;
PI WPI, 1995-098757/13.
DR N-PSDB; AAQ83963.
XX
XX
PT DNA coding for fructose-6-phosphate 1-phosphotransferase - of
PT plant origin, for prodn. of transformant plant cells with altered
PT sugar content
XX
XX
PS Claim 6; Page 39-43; 79pp; Japanese.
XX
XX The amino acid sequence of the novel ATP-dependent fructose-6-phosphate
CC 1-phosphotransferase enzyme (BC 2.7.1.11; PFX) encoded by the Flavaria
CC brownii gene PFX-FBI. Plants transformed with these genes can express
CC the enzyme. The transformed plants can produce varieties that have
CC altered sugar content on storage at low temperatures.
CC (Updated on 25-MAR-2003 to correct PN field.)
SQ Sequence 483 AA;

XX Hiyoshi T, Kasaoka K, Mine T, Page MJA, Tyson HR;
 XX WPI; 1995-098757/13.
 DR N-PSDB; AAQ85986.
 XX
 PT DNA coding for fructose-6-phosphate 1-phosphotransferase - of
 PT plant origin, for prodn. of transformant plant cells with altered
 PT sugar content
 XX
 PS Claim 11; Page 58-61; 79pp; Japanese.
 XX
 CC The amino acid sequence of the novel ATP-dependent fructose-6-phosphate
 CC 1-phosphotransferase enzyme (EC 2.7.1.11; PFK) encoded by the Raphanus
 CC sativus (radish) gene, pPFK-RS1. Plants transformed with genes encoding
 CC PFK (see AAQ85982-86) can express the enzyme. The transformed plants
 CC can produce varieties that have altered sugar content on storage at low
 CC temperatures.
 CC (Updated on 25-MAR-2003 to correct FN field.)
 CC
 SQ Sequence 426 AA;
 Query Match 11.5%; Score 263; DB 16; Length 426;
 Best Local Similarity 25.8%; Pred. No. 5.1e-16;
 Matches 108; Conservative 65; Mismatches 173; Indels 72; Gaps 17;
 QY 37 ILTAGLAPCLNSAIGSLIERTEIDPSIEICRGYKGLLDSDSYVAEYKKAQVL 96
 DB 50 IVTGGTLPGLMTVIRREIVCGLSYVYGVKLLGIBGGRGYAANTLDL--KTVNDI 106
 QY 97 QRFGGSVIGNSRVKLTNVKDCVKRGLYEGEDPQKVAADQLVMDVILHTIGDDTNTA 156
 DB 107 HKRGITIGTSR-----CGHDTTKI--VDSIQRGINQVYIIGDGSQNG 149
 QY 157 AADLAAPLARNYGLTVGLPKTVNDVFPKQSLGATTAEGAKRFPMNVANANPR 216
 DB 150 AAVIFEIRRRGLKVAAGIKPTIDNDIPIDRSFGDTAVEAQRANAAHVATSFEN 209
 QY 217 MELIYEVKRNCGMLTAATAOEYKRLDRAEMPELGLTRSEYVHAFVEMADIEAB 276
 DB 210 GIGLVKLMKRGYSGLPAM-----YARLASR-----DYDCLIPESFFLEGR 250
 QY 277 -----AKRLREYADKVDQCNITFVSGAGVEAIVAEQAKQGEVPRDPAFGHITLDAVNP 329
 DB 281 GGLFEFLIKRLKEIGHNV-----IVIAEGAG--QDLIAESNEQSTTL--KDAAGNKLLQDV-- 302
 QY 330 GKMPGEQGNMGITGAETLVOK--SGYFAPASASNVDMRLIKSCADLAVECAFRRESGV 386
 DB 303 GLMTISQRIKDHPAKKMTINLKYIDFTYIRAVPSNASD---NVCTLLAQSAVH---GV 355
 QY 387 I-GHDEDNQNVLRA-----IEPPRI--KSGKPFNIDTWMNSMLSEIQPKGKYAVSH 437
 DB 356 MAGVNGFVGLVNGHTYIPYRITRKQNKVITDRMAR--TLSTNQPSMKDDHH 412
 RESULT 10
 AAR71579 ID AAR71579 standard; Protein; 485 AA.
 XX
 XX AAR71579;
 XX
 XX 25-MAR-2003 (updated)
 XX 11-OCT-1995 (first entry)
 XX
 XX Solanum tuberosum fructose-6-phosphate 1-phosphotransferase.
 XX
 XX ATP-dependent fructose-6-phosphate 1-phosphotransferase enzyme; plant;
 XX potato; Solanum tuberosum; rice; Oryza sativa; maize; Zea mays; radish;
 XX Raphanus sativus; Flaveria brownii; primer; expression vector;
 XX Agrobacterium tumefaciens; sugar; storage; temperature.
 XX
 XX Solanum tuberosum.
 OS
 XX

PN WO9505457-A1.
 XX
 XX 23-FEB-1995.
 XX
 XX 16-AUG-1994; 94WO-JP01352.
 XX
 XX 19-AUG-1993; 93JP-0226454.
 XX
 XX (NISB) JAPAN TOBACCO INC.
 PA
 XX Hiyoshi T, Kasaoka K, Mine T, Page MJA, Tyson HR;
 XX WPI; 1995-098757/13.
 DR N-PSDB; AAQ85982.
 XX
 PT DNA coding for fructose-6-phosphate 1-phosphotransferase - of
 PT plant origin, for prodn. of transformant plant cells with altered
 PT sugar content
 XX
 PS Claim 4; Page 33-37; 79pp; Japanese.
 XX
 CC The amino acid sequence of the novel ATP-dependent fructose-6-phosphate
 CC 1-phosphotransferase enzyme (EC 2.7.1.11; PFK) encoded by the potato
 CC (Solanum tuberosum) gene pFK32. The DNA sequence was isolated from a
 CC potato cDNA library using primers AAQ85987-91. The sequence was used to
 CC construct the plant expression vector pPFK(35S) which was transformed
 CC into potato plants (Bintje variety) via Agrobacterium tumefaciens. The
 CC transformed plants can express the enzyme and produce plant varieties
 CC that have altered sugar content on storage at low temperatures.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 485 AA;
 Query Match 11.5%; Score 262; DB 16; Length 485;
 Best Local Similarity 25.7%; Pred. No. 7.8e-16;
 Matches 113; Conservative 56; Mismatches 179; Indels 92; Gaps 17;
 QY 7 YHLLADIRCFHWFLENFNYTLNKKPKVAILTAGLAPCLNSAIGSLIERTEIDPSIE 66
 DB 86 YFSGDDVAC-----IVTCGLCPGLMTVIRREIVHSLDYMGVNK 125
 QY 67 ILCRGYKGLLDSDSYPTAEVRKKAQVLQKSGSVIGNSRVKLTNVDCVARGLVKSG 126
 DB 126 VFGIDGTYRFPYSKNTINLTP--KTVNDIHKRGITLSSR-----GG 166
 QY 127 EDPQVAADQLVMDVILHTIGDDTNTAADLAAPLARNYGLTVGLPKTVNDVFP 186
 DB 167 HDITTKI--VDSIQREINQVYIIGDGTQKGAIVIEIRRRGLKTVAGIPKTIIDIPV 225
 QY 187 IKOSLGAMTAEGAKRFPMNVANANPRMLIVHEVNGRNCGMLTAATAOEYKRLDRA 246
 DB 226 IDRSFGDTAVEAQRANAAHVAEASANGIGVVKLMRGYSGLPIA----- 271
 QY 247 EMLPELGLTRSEYVHAFVEMADIEAB-----KRLREYADKVDQCNITFVSGAG 299
 DB 272 -----MYATLASNDVDLCLIPESFFLEBDGGLFEYIRKLENGHNV-----IVIAEGAG 332
 QY 300 VEATVAB--NQAKQGEVPRDPAFGHITLDAVNPGEKMFGEQFQAQMTGAETLVQ-----KSG 352
 DB 323 QELIAEENNAKNEQ--DASGKLLQDV--GLMTISQRIKDH-ARTKMPITLKYIDPT 376
 QY 353 YFAPASASNVDMRLIKSCADLAVECAFRRESGVIGHDED--NGNVLRAIEFPRIKSGKP 410
 DB 377 YMIRAVPSNASDN---VYCTLLAQSCVHAGMAGYTGFTSGLVNGR--QYIIPFRITRKQV 432
 QY 411 FNITVD--WFSNMLSEIQP 428
 DB 433 MYVITDRMAR--TLSTNQP 451
 RESULT 11
 ABB93109 ID ABB93109 standard; Protein; 500 AA.
 OS

XX	AC	AB93109;
XX	DT	31-MAY-2002 (first entry)
XX	DE	Herbicidally active polypeptide SEQ ID NO 2320.
XX	KX	Herbicidal; plant; agriculture; herbicide.
XX	OS	Arbidopsis thaliana.
XX	FN	MO200210210-A2.
XX	PD	07-FEB-2002.
XX	PF	28-AUG-2001; 2001WO-BP09892.
XX	PR	28-AUG-2001; 2001WO-EP09892.
XX	PA	(PARB) BAYER AG.
XX	PI	Tietjen K. Weidler M;
XX	DR	WPI; 2002-269010/31.
PT	PT	Identifying plant target proteins for herbicidally active compounds,
PT	PT	comprising aligning and comparing nucleic acid or amino acid sequences
PT	PT	from plant with nucleic acid or amino acid sequences from non-plant
PT	PT	organisms -
PS	PS	Claim 5; SEQ ID NO 2320; 26tpp + Sequence listing; English.
XX	CC	The invention relates to identifying target proteins
XX	CC	(AB990790-AB994016) for herbicidally active compounds, comprising
XX	CC	aligning and comparing nucleic acid or amino acid sequences from plant
XX	CC	with nucleic acid or amino acid sequences from non-plant organisms using
XX	CC	suitable search parameters, where plant sequences having an E-value
XX	CC	greater by a factor of 3 than the E-value of most similar non-plant
XX	CC	sequences are selected. The polypeptides or nucleic acids encoding them
XX	CC	are useful for identifying modulators. The identified modulators are
XX	XX	useful as herbicides.
SQ	SQ	Sequence 500 AA;
Query Match	11.3%; Score 257.5; DB 23; Length 500;	
Best Local Similarity	25.6%; Preq. No. 2,2e-15;	
Matches 109; Conservative 59; Mismatches 167; Indels 91; Gaps 16;		
CY	37 ILTAGGLAPCNSAIGSL-----IEREIDPSIEIIC-----YRGGYKLL 78	
DB	92 IVTGGCLPGANTVIREIVSSLSWTGKYRILGIVS--FDCCLLTKTNTYGTRGFY 148	
CY	79 LGSYPVTAVERKKAGVLORFGGSVIGNSRVQLTNVKDCYRKGLVKSGEDPOKVAAOLV 138	
DB	149 AKMTVSLSDSKY---VNDIHKKGSTLIGTSR-----GGHDTYKI-VDSIQ 188	
CY	139 KDGVDLITFTIGSDDDNTMAAADLAALANNNYLTLYGLPKTYNDNVFPFKSIGAWTAAE 198	
DB	189 DRGINQVYIIIGDGTOQRGAISVFEEIRRRGLNVAVIGIKTIINDIPVIDNSFGFDIAVE 248	
CY	199 QGARFYNNVVAVENNANPMRLIVHEWGNGNCMLTATATQEVKRLDRAEWLPBLGLTREES 258	
DB	249 EAQRAINAHAEAESIEINGIVKLMGRYSGITA-----MYATLAS 289	
CY	259 YEYNAVFPPEMAIDLEEA-----KALREMDKYVCNMFVSGAGYEALVAMOKG 311	
DB	290 RDVDCCLPESFPYIEGEGGLEFEYTEKRKEKSGHNV---LVLAGAQQDILMSKSMEEM- 344	
CY	312 QEVPPDAIGHIILDVNEQKPFGCEQFAQMIGAETLVQ-----KSGYFARASANYDMRL 367	
DB	345 --TLMDASGNKLKLV--GLMWSQSIKHFFNQKRVVMNLXYIDFTYIMRAYVSNASDAYV 400	
CY	368 IKSCADLAVECAFRESGYTGDEDONGNV---LRAIERPRIKGGKPPFIIDD--WFNSML 422	

Db	401	CTLLA	SNHG	MA	GT	TV	-----	SG	LV	NR	Q	RT	Y	IP	PR	IT	K	Q	NR	IV	IT	D	RR	MA	-	LL	454
Qy	423	SETGP	428																								
Db	455	SSINP	460																								
RESULT 12																											
ID	AA636438																										
ID	AA636438	standard; Protein, 473 AA.																									
XX	AA636438;																										
AC	AA636438;																										
XX	18-OCT-2000	(first entry)																									
DT	18-OCT-2000	(first entry)																									
XX	Arabidopsis thaliana	protein fragment SEQ ID NO: 44655.																									
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 44655.																									
XX	Protein identification; signal transduction pathway; metabolic pathway;																										
KW	hybridisation assay; genetic mapping; gene expression control; promoter;																										
KW	termination sequence.																										
XX	Arabidopsis thaliana.																										
OS	Arabidopsis thaliana.																										
XX	BP1033405-A2.																										
PN	BP1033405-A2.																										
XX	06-SEP-2000.																										
PD	06-SEP-2000.																										
XX	25-FEB-2000;	2000RP-0301439.																									
PR	25-FEB-2000;	2000RP-0301439.																									
XX	25-FEB-1999;	99US-0121825.																									
PR	05-MAR-1999;	99US-0123180.																									
PR	09-MAR-1999;	99US-0123548.																									
PR	23-MAR-1999;	99US-0125788.																									
PR	25-MAR-1999;	99US-0126264.																									
PR	29-MAR-1999;	99US-0126785.																									
PR	01-APR-1999;	99US-0127462.																									
PR	06-APR-1999;	99US-0128234.																									
PR	08-APR-1999;	99US-0128714.																									
PR	16-APR-1999;	99US-0129845.																									
PR	19-APR-1999;	99US-0130077.																									
PR	21-APR-1999;	99US-0130449.																									
PR	23-APR-1999;	99US-0130510.																									
PR	28-APR-1999;	99US-0130891.																									
PR	30-APR-1999;	99US-0131449.																									
PR	30-APR-1999;	99US-0132048.																									
PR	04-MAY-1999;	99US-0132407.																									
PR	05-MAY-1999;	99US-0132484.																									
PR	06-MAY-1999;	99US-0132485.																									
PR	07-MAY-1999;	99US-0132486.																									
PR	11-MAY-1999;	99US-0132487.																									
PR	14-MAY-1999;	99US-0132486.																									
PR	14-MAY-1999;	99US-0134218.																									
PR	14-MAY-1999;	99US-0134219.																									
PR	14-MAY-1999;	99US-0134221.																									
PR	14-MAY-1999;	99US-0134370.																									
PR	18-MAY-1999;	99US-0134768.																									
PR	19-MAY-1999;	99US-0134941.																									
PR	20-MAY-1999;	99US-0135124.																									
PR	21-MAY-1999;	99US-0135553.																									
PR	24-MAY-1999;	99US-0135629.																									
PR	25-MAY-1999;	99US-0136021.																									
PR	27-MAY-1999;	99US-0136392.																									
PR	28-MAY-1999;	99US-0136782.																									
PR	01-JUN-1999;	99US-0137222.																									
PR	03-JUN-1999;	99US-0137528.																									
PR	04-JUN-1999;	99US-0137562.																									
PR	07-JUN-1999;	99US-0137724.																									
PR	08-JUN-1999;	99US-0138094.																									
PR	10-JUN-1999;	99US-0138540.																									
PR	10-JUN-1999;	99US-0138847.																									
PR	14-JUN-1999;	99US-0139119.																									

QY 97 QRFSSVIGNSRVKLTNVKOCVKEGVLKEGEDPOKVAADQVVDVLIHTIGDDDTNTA 156
 Db 154 HRSGLTIGTSR-----GGHNTTKI-VDSIQDRGINQVYIIIGDSSQKG 196
 QY 157 AADLAFLARNNGVLTIGLPTVDNDVFPKISLGAMTAAGAGAFPMNVVAENNANPR 216
 Db 197 AAALFEIRKRLKLVAVAGIPKTIIDNDIPIDRSFGPDVAEBAQAINAAHAEASFEN 256
 QY 217 MLIVHEWGRNGCMLTLTAQOYRKLDRBAEWLPELGITRESYEVHAFVPEPAIDLEAE 276
 Db 257 GIGLVKMGRTYSGFLA-----MHATLASRDVDCCLIPESPFLEBS 297
 QY 277 A-----KRLREWDEKDCVNIPESEGAGVAIWAEMQAGQVPRDAPGHIKLDAVNP 329
 Db 298 GGLFEPIIDKRLKESGHN-----IYIAEGAGDILSESM--KESTTLKDSGKLLDID-- 349
 QY 330 GKMFEGQFAOMIGAEKTLVQK--SGYFAPASASNVDDMLIKSCADLAVECAFRESGCV 386
 Db 350 GLWISQRIKDHFAKQMTLTKYIDPTYMIRAVPSNAD---NVCCTLLAQSAVH--GV 402
 QY 387 I-GHDEDNENVLRA-----IEPPRI--KGKFPNIDTDWNSMLSEIGOP 428
 Db 403 MAGTNGFTVGLVNGRHTYIPFNRIITEKONKVVITDRMAAF-LLSSTNQP 450

RESULT 13

ABB93145
 ID ABB93145 standard; Protein: 473 AA.
 AC ABB93145;
 XX
 XX 31-MAY-2002 (first entry)
 DE Herbicidally active polypeptide SEQ ID NO 2356.
 XX
 XX Herbicidal; plant; agriculture; herbicide.
 XX
 XX Arabidopsis thaliana.
 XX
 XX W0200210210-A2.
 XX
 XX 07-FEB-2002.
 XX
 XX 28-AUG-2001; 2001MO-EP09892.
 XX
 XX 28-AUG-2001; 2001MO-EP09892.
 XX
 XX (FARB) BAYER AG.
 PA
 XX Tietjen K, Weidler M;
 PI
 XX WPI; 2002-269010/31.
 DR
 XX
 XX
 PT Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms -
 PT
 XX
 XX
 PS Claim 5; SEQ ID NO 2356; 261bp + Sequence Listing; English.
 XX
 XX The invention relates to identifying target proteins
 CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
 CC aligning and comparing nucleic acid or amino acid sequences from plant
 CC with nucleic acid or amino acid sequences from non-plant organisms using
 CC suitable search parameters, where plant sequences having an E-value
 CC greater by a factor of 3 than the E-value of most similar non-plant
 CC sequences are selected. The polypeptides or nucleic acids encoding them
 CC are useful for identifying modulators. The identified modulators are
 CC useful as herbicides.
 CC
 XX
 XX Sequence 473 AA;
 SQ

Query Match 11.0%; Score 251; DB 23; Length 473;

Best Local Similarity 25.2%; Pred. No. 8,2e-15;
 Matches 103; Conservative 60; Mismatches 174; Indels 72; Gaps 15;

QY 37 ILTAGGLADCLNSAGLSLIERYTEIDPSIEIICYRGYGLLIGDSYPYAEVRKZAGYL 96
 Db 97 IYVGGCLGLMTVIEIYVIGLSYVWGVRILIGIDGEGFVARNTHLDL--KTVNDI 153
 QY 97 QRFSSVIGNSRVKLTNVKOCVKEGVLKEGEDPOKVAADQVVDVLIHTIGDDDTNTA 156
 Db 154 HRSGLTIGTSR-----GGHNTTKI-VDSIQDRGINQVYIIIGDSSQKG 196
 QY 157 AADLAFLARNNGVLTIGLPTVDNDVFPKISLGAMTAAGAGAFPMNVVAENNANPR 216
 Db 197 AAALFEIRKRLKLVAVAGIPKTIIDNDIPIDRSFGPDVAEBAQAINAAHAEASFEN 256
 QY 217 MLIVHEWGRNGCMLTLTAQOYRKLDRBAEWLPELGITRESYEVHAFVPEPAIDLEAE 276
 Db 257 GIGLVKMGRTYSGFLA-----MHATLASRDVDCCLIPESPFLEBS 297
 QY 277 A-----KRLREWDEKDCVNIPESEGAGVAIWAEMQAGQVPRDAPGHIKLDAVNP 329
 Db 298 GGLFEPIIDKRLKESGHN-----IYIAEGAGDILSESM--KESTTLKDSGKLLDID-- 349
 QY 330 GKMFEGQFAOMIGAEKTLVQK--SGYFAPASASNVDDMLIKSCADLAVECAFRESGCV 386
 Db 350 GLWISQRIKDHFAKQMTLTKYIDPTYMIRAVPSNAD---NVCCTLLAQSAVH--GV 402
 QY 387 I-GHDEDNENVLRA-----IEPPRI--KGKFPNIDTDWNSMLSEIGOP 428
 Db 403 MAGTNGFTVGLVNGRHTYIPFNRIITEKONKVVITDRMAAF-LLSSTNQP 450

RESULT 14

AAG36437
 ID AAG36437 standard; Protein: 537 AA.
 AC AAG36437;
 XX
 XX 18-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 44654.
 XX
 XX
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.
 XX
 XX Arabidopsis thaliana.
 OS
 XX
 XX EP103405-A2.
 PN
 XX
 XX
 XX 06-SEP-2000.
 PD
 XX
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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Search completed: January 29, 2004, 14:36:32
 Job time : 48 secs

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 Db 361 NVDDMRLLKSCADLAVECAFRRSGVIGHDENGNVALEFPRIKGGKPNITDWMNS 420
 Qy 421 MLSTIGQPKGKGVESH 437
 Db 421 MLSTIGQPKGKGVESH 437

RESULT 2
 US-08-416-870C-4
 Sequence 4, Application US/08416870C
 Patent No. 5824862

GENERAL INFORMATION:
 APPLICANT: HIYOSHI, TORU
 APPLICANT: MINE, TOSHIKI
 APPLICANT: KASAKA, KEISUKE
 APPLICANT: TYSON, ROBERT HUM
 APPLICANT: PAGE, ANTHONY MILES JOHN
 TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
 TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECT
 TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UND
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 STREET: PO BOX 747
 CITY: FALL CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,870C
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 760-195P(PCT)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 483 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-416-870C-4

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 Qy 329 PKRMFGEO-----PAQMTGAKTIVQ-KSGYFARASASNDMDRLIKSCDLAVECAFRR 383
 Db 349 -GLMISDKIKAFPAKIPMPETILTKYIDPYMIRAVPSNASDN--VYCTLLAQSCVHGV 404
 Qy 384 SGVIGHDED--NGNVLRALEFPRIKGGKPNITD--WFSMLSEIGOP 428
 Db 405 AGTGTSTGLVNGR-QTYIFNRITRKQNNVYITDMMAR-LLSTINOP 451

RESULT 3
 US-08-416-870C-6
 Sequence 6, Application US/08416870C
 Patent No. 5824862

GENERAL INFORMATION:
 APPLICANT: HIYOSHI, TORU
 APPLICANT: MINE, TOSHIKI
 APPLICANT: KASAKA, KEISUKE
 APPLICANT: TYSON, ROBERT HUM
 APPLICANT: PAGE, ANTHONY MILES JOHN
 TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
 TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECT
 TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UND
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 STREET: PO BOX 747
 CITY: FALL CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,870C
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY JR, GERALD M
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 760-195P(PCT)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 469 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-416-870C-6

Query Match 11.6%; Score 264.5; DB 2; Length 469;
 Best Local Similarity 26.8%; Pred. No. 1.9e-17;
 Matches 109; Conservative 56; Mismatches 173; Indels 69; Gaps 16;
 Qy 37 ILTAGGLAPCLNSALISLIERYTEIDPSIRICRYRGYKGLLDSDYPTVAEVRKAGV 96
 Db 74 IITAGGLAPCLNTVIRIIVGGLANDMGVSKVLIGGGRGFVACNTIDLSF--KSVNDN 130
 Qy 97 QRFSGSYIGNSRKLTNNVNDQVKGGLVKEGSDQYAAADQLVNDQVDLHTTIGDDPTNTA 156
 Db 131 HKRGGTVLIGTSR-----GGHDKPKI-VDSIQRGINQVYIIGSDGTQK 173
 Qy 157 AAADLAALARNRYLTGPKTYDNDVFPKQSLGKWTAAEGCARFNNVAVANNANP 216
 Db 157 AAADLAALARNRYLTGPKTYDNDVFPKQSLGKWTAAEGCARFNNVAVANNANP 216

Db 174 AGVIFERIRRGKLVAVAGIPRTIDNDIPVLDSPFGDFAVEAQAIRNAAYEASAAEN 233
 Qy 217 MLIVHEVNGNCGMIFAAATQAEYKLLDRAMLPBGLTSEYEVNAVPEMAIDLEAE 276
 Db 234 GIGLVKLNHSGFIA-----HYATLASR-----DVDCCLPESPPTLEGE 274
 Qy 277 A-----KELREYMDKVCVNI FVSEAGVEAI VAEQAKGOEVPDAPGH-IKLDAYN 328
 Db 275 GGLFVYLEKLEKENGHNV-----IVVAGAGQKLIINFKESMG-----KDAAGNSITLDDV-- 324
 Qy 329 PKRMFGQEPQMTIGAKETLVQ---KSGYFARASASVNDMLIKSCADLAVECARRES 384
 Db 325 -GLMISQKIREHFQKIKTTINLKXIDPTVMIRAI PSNASDNYCTLLARVAGAGAGYT 383
 Qy 385 G-VIGHEDNGNVLAIEPPI--KSGKPFNIDTWNMSLSEIGP 428
 Db 384 GFTVG--QVNGRHC-VTFYRIRKQKVSITDRMAR-LISSTNDP 426

RESULT 4

US-08-416-870C-2

Sequence 2, Application US/08416870C

Patent No. 5824862

GENERAL INFORMATION:

APPLICANT: HIYOSHI, TORU

APPLICANT: MINE, TOSHIKI

APPLICANT: KASAKA, KEISUKE

APPLICANT: TYSON, ROBERT HUM

APPLICANT: PAGE, ANTHONY MILES JOHN

TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE

TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTO

TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP

STREET: PO BOX 747

CITY: FALL CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/416,870C

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR, GERALD M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 760-195P (PCT)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 485 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-416-870C-2

Query Match 11.5%: Score 262; DB 2; Length 485;
 Best Local Similarity 25.7%: Pred. No. 3.4e-17;
 Matches 113; Conservative 56; Mismatches 179; Indels 92; Gaps 17;

Qy 7 YHLTADIRFGHPLNENFYTLNMRKPKVAILTAGGLAPCLNSAGSLIRRYTEIDPSIE 66
 Db 86 YFSSDDVRAE-----IVTCGGLCPGLNTVYIEIVHSLDVMYGVNK 125

Qy 67 IICVGGYKGLLADGSPYVTAEEVRKAGVLOFQSGSVIGNSVYKLTNNVQCVKGLVRE 126
 Db 126 VFGIDGGRGFGYSKNIMLTP---KTVNDIHRGGTILGSSR-----CG 166
 Qy 127 EDPQKAVDQVQKGVVDLHTIGEDDTFAADLAAFLARNNYGLTVGLPXTVNDVPE 186
 Db 167 HPTTGI-VDSIODRIRINQYIIIGDGTQGAIVYIEIRRLKVIAGIPTITNDIPV 225
 Qy 187 IKOSIGAVTAEGQARYENQVVAENNANPRMLIVHEVNGNCGMTLAATQAEYKLLDRA 246
 Db 226 IKSFGPDTAVEAQAIRNAAYEASAAENGVKNGRYSGFIA----- 271
 Qy 247 EMLPELGLTRESYEVNAVPEMAIDLEAE-----KELREYMDKVCVNI FVSEAG 299
 Db 272 -----MYATLASRDVLCILPESPYLEGGGLFEYIERKLENGHNV-----IVVAGAG 322
 Qy 300 VEATVAAE-MQAKGOEVPDAPGHIKLDVNPQKMGEOQAMIGAKETLVQ-----KAG 352
 Db 323 QELIABENNAKNEQ---DASGNKLLQV--GLMISQKIRDF-ATKTMPTITLKIDPT 376
 Qy 353 YFARASASVNDMLIKSCADLAVECARRESGVIQHDG--NGNVLAIEPPIKSGRP 410
 Db 377 YMIRAVPSNASDN---VYCTLLAQSCVHAGAGYGTGSLVNGR-QTYIPIRIRIKQN 432
 Qy 411 FNIQDT--WFNSMLSEIGP 428
 Db 433 KVVITDRMAR-LISSTNDP 451

RESULT 5

US-08-416-870C-10

Sequence 10, Application US/08416870C

Patent No. 5824862

GENERAL INFORMATION:

APPLICANT: HIYOSHI, TORU

APPLICANT: MINE, TOSHIKI

APPLICANT: KASAKA, KEISUKE

APPLICANT: TYSON, ROBERT HUM

APPLICANT: PAGE, ANTHONY MILES JOHN

TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE

TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTO

TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP

STREET: PO BOX 747

CITY: FALL CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/416,870C

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR, GERALD M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 760-195P (PCT)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 426 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-416-870C-10

Query Match 11.4%; Score 260; DB 2; Length 426;
 Best Local Similarity 25.6%; Pred. No. 4.4e-17;
 Matches 107; Conservative 65; Mismatches 174; Indels 72; Gaps 16;

37 ILTAGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDSDSPVTAERKAGVL 96
 50 IVTCGGLOPGLNTVIREIVCGLSYMGVYKILIEGGGREGFARNTIDLDL---KTVNDI 106
 97 QRFSGVIGNRVYKLTNWKDCVKGKGLVKEGEDPQVNAADQLVKDGVDILHTIGDDTNTA 156
 107 HKRGSTILGSTR-----GGDDTTKI-VDSIQDGINQVITIGEDSQKG 149
 157 AADLAFLARNNGVLTGPKTYDNDVFPKISGLAMTAEGGARVPANVAENNA 216
 150 AAVIFERRRGLKVAVAGIKPTIDNDIPIDRSFGPDTAEEAKAINAHVATSPEN 209
 217 MLIVHEVNRGCGWLTATAEYKRLDRAEWLDELITRESYEVHAFVPEMAIDLEAE 276
 210 GILVKLMGRYSGLFA-----MATLASRDVDCCLIPESPFLEK 250
 277 -----AKRLREVNDKVCVNI FVSBGAGVEALVAEQAGVEPPDAFGHKLDAVNP 329
 251 GGLFEPICKRLKEIGHNV---IVYABAG-QDLAASNEGSTTL-KDASGNKLQCV-- 302
 330 GKATGEGQAPQNTGAEKTLVOK---SGFPARASASNVDMRLKSCADLAVECAFRESGV 386
 303 GLMTSQRKIDHFAKRMKTLMLKYIDETVMIRAVPSNAD---NVCCTLAQSAVH---GV 355
 387 I-GHEDENGVTLRA---IEPPRI--KGKGFENIDTWMFNSMLSEIGCPKRGYVASH 437
 356 MAGINGFTVGLVNGRHITIPRYITEKONKVVITDRMAR-LISSTQPSMKDDDH 412

RESULT 6
 US-09-134-001C-3774
 Sequence 3774, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 3774
 LENGTH: 345
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3774

Query Match 9.9%; Score 226.5; DB 4; Length 345;
 Best Local Similarity 25.4%; Pred. No. 5.3e-14;
 Matches 105; Conservative 68; Mismatches 136; Indels 105; Gaps 19;

26 YTLNPKPKKVALITAGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDSDSPV 85
 21 YVVM---KKIAVLITSGSGSPGEMAAVRAVTR-TAIVNNIEVYGVGYGGLDDDDTHKL 75
 86 TAEVRKAGVLRQFSGSVIGNSRVYLTNVKDCVKGKGLVKEGEDPQVNAADQLVKDGVDIL 145
 76 --ELGSDVDTIQR-GGTFLFSAR-----CPQ---FKE-EDVRKKAILEMLRKGIGEL 120
 146 HTIGGDDTNTAADLAFLARNNGVLTGPKTYDNDVFPKISGLAMTAEGGARVPANVAENNA 205
 121 VVIGDGSYRGAGQISEBCKE---IQTIIGPTIDNDINFTDPTIGFIDA-----L 168
 206 NVVALEN-----NANRMLIVHEVNRGCGWLTATAEYKRLDRAEWLDELITRES 257

Db 169 NTIIEVDKIDRTASSHARTFIV-EVWMDCG-----DLALW---AGI----- 207
 QY 258 SYEVHAFVPEMAIDLEAEKRLREVNDKVCVNI FVSBGAGVEALVAEQAGVEPPDA 317
 Db 208 SVAGETIVPEVNTDVKDAEKEIGIKGKXHSI-----VVAEGCMSGQCADE 258
 QY 318 AFCHIKLDAVNPQKMGEGEPQNTGAEKTLVOKSGYFPARASASNVDMRLKSCADLAVE 377
 Db 259 LTKYINID-----TRVSLGSHIQGGSPSGADRYLASRLGAYAVE 298
 QY 378 CAFRES-----GYIGHDENGVTLRAIEPPRI-KGKGFENIDTWMFNSMLSEIGC 427
 Db 299 LKQGTANGVGL-----RNQVLSTPDEI-----FAESDRKKNQMTLAK 341

RESULT 7
 US-09-107-532A-6470
 Sequence 6470, Application US/09107532A
 Patent No. 6583275
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSER: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Atinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 6470:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 323 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc. feature
 LOCATION: (B) LOCATION 1...323
 SEQUENCE DESCRIPTION: SEQ ID NO: 6470:
 US-09-107-532A-6470

Query Match 9.4%; Score 215.5; DB 4; Length 323;
 Best Local Similarity 24.4%; Pred. No. 6.9e-13;
 Matches 94; Conservative 56; Mismatches 114; Indels 121; Gaps 17;

33 KKVAILTAGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLDSDSPVTAERK 92

DQ 5 KRIGILTSGDAPGMAAFAVVR-----KGIYGL-----EV 37
 QY 93 AGYLORFGSGVGN-SRVLKLTNWKDCVKG-----LVKGEDEPQKVAADOLYK 139
 DB 38 YGINVGAGIADIRLDAVDGDKIQFGSTFLYSARYPEPATEEG---QLNGISQLKK 94
 QY 140 DGDVILITGGDDNTTAADLAFLANNGLTVIGLPRKVDVPPFKISLGANTMAEQ 139
 DB 95 FGIJGLVVIIGDSSYHGA-----MALTKRGPAVVGIPGTDIDIPDTDFTIGFDTA--- 145
 QY 200 GAEFNVVAEN-----NANPMLIVHEVGRNCGMLTAADQERYKLDRAEMLPE 251
 DB 146 -----INTVESIDRIKDPTASHRTFVL-EVMGRNAG-----DIALMSGV 185
 QY 252 LGLTRESEYHAAVFPFPMALDLEAKKLEAYMD--KDCVNI FVSEGAIVEALVAMQ 309
 DB 186 AGGADG-----IIPHPDPMASVAKKIQEGRDRGKGLT-LTLEAG----- 226
 QY 310 KGGVPRDAFGHIKLDVNPCKWFGBOFQOMIGABKTLVQSGYFAPASAVDMLIK 369
 DB 227 -----VMGNEFAEGLSE-FQDYHTRVSLGHVYVAGAPASARDVMA 268
 QY 370 SCADLAVECAFRBSGV-IG-HDED 392
 DB 269 KFGAVAVELLQEGKGLCVGIHNE 293

RESULT 8
 US-08-416-870C-8
 ; Sequence 8, Application US/08416870C
 ; Patent No. 5824862

; GENERAL INFORMATION:
 ; APPLICANT: HIYOSHI, TORU
 ; APPLICANT: KASNOKA, KEISUKE
 ; APPLICANT: TYSON, ROBERT HOW
 ; TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
 ; TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTO
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 ; STREET: PO BOX 747
 ; CITY: FALL CHURCH
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/416,870C
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURPHY JR, GERALD M
 ; REGISTRATION NUMBER: 28,977
 ; REFERENCE/DOCKET NUMBER: 760-195P(PCT)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 205-8000
 ; TELEFAX: (703) 205-8050
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 522 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-416-870C-8

Query Match 9.3%; Score 211.5; DB 2; Length 522;

Best Local Similarity 23.7%; Pred. No. 3,6e-12;
 Matches 98; Conservative 69; Mismatches 168; Indels 75; Gaps 15;

QY 34 KVALTAGGLAPCLNSAIGSLIERYTEIDPSIEIC-----YRGCV-KGLLGDSPVTA 87
 DB 166 KVALITCGGLCPGLNDVIRQIV--FTLEHYGVKNI VGI FPGYRGFEKGL---KEMPLSR 220
 QY 88 EVRKAGVLPFGSSVIGNSRYKLTVNDCVYKGLVKGGEDEPQKVAADQLYKGDVILHT 147
 DB 221 DVEN-----INLSGSGFLG-----VARGAKTSE-----IVSIOARRIDMFEV 260
 QY 148 IGGDDNTTAADLAFLANNGLTVIGLPRKVDVPPFKISLGANTMAEQARFPMV 207
 DB 261 IGGNSHAGANAIHEECRKLKVSVAVPEKTDIDIPMDKTFGDTIVESAQRINSA 320
 QY 208 VANNANPMLIVHEVGRNCGMLTAADQERYKLDRAEMLPBGLTRESYHAAVFP 267
 DB 321 YIERSAVHIGLVLTLMGSSGFIA-----MHASLSGQIDVCLIP 361
 QY 268 EWAIDLEAKKLEAYMDKVD---CVNIFVSEGAIVEALVAMQKGOEVRDARFHIK 323
 DB 362 EVSFTLDEHGVLRHLEHLNTRGFCV-VCAVEGAGQDL-----QSNATDASGVY 413
 QY 324 IDAVNPCKWFGBOFQOMI-----GAEKLTVQSGYFAPASAVDMLIKSCADL 374
 DB 414 LSD-----FGVHMQKIKKHFKDQIGPADLKYIDPT-YMVAACRANSDALICTVLGN 466
 QY 375 AVECAFRBSGVIGHEDNGVLAIRPFRKIGKPRNIDTFNSMLSEIGOP 428
 DB 467 AVHGAFAFGPSGITSGVCTHYVYLPIT-EVITTPHVNPNSMWRCLTSTQOP 519

RESULT 9

US-08-280-690-2
 ; Sequence 2, Application US/08280690

; GENERAL INFORMATION:
 ; APPLICANT: Mansour, Tag B
 ; TITLE OF INVENTION: Compositions, Treatments, and
 ; TITLE OF INVENTION: Diagnostics for Schistosomiasis and Related Diseases
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward
 ; STREET: 5 Palo Alto
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306-2155
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/280,690
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Nealey, Richard L
 ; REGISTRATION NUMBER: 30,092
 ; REFERENCE/DOCKET NUMBER: STAN-141/00US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-843-5070
 ; TELEFAX: 415-857-0663
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 781 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-280-690-2

US-09-198-452A-458
 ; Sequence 458, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Giffels, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO 458
 ; LENGTH: 845
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; US-09-198-452A-458

Query Match 5.0%; Score 113.5; DB 4; Length 845;
 Best Local Similarity 21.5%; Pred. No. 0.033;
 Matches 117; Conservative 73; Mismatches 170; Indels 185; Gaps 30;

QY 30 NEDKXVALTAG--LAPCLNSAGSLIERYTEIDPSIBIIICRGYKGLLDGSPYPT 86
 DB 179 DKBEKLSALTAHYDLEMTREKLDVYGRSEVERIILICRRKNNPVLIG----- 233
 QY 87 AEVRKA--GVLORFGSVIGNSRYKLTVKDCVR-----GLVKEGDEPQ 130
 DB 234 AGVKATIAVGLAQ-----KIIINEVPDLARKKLLITDLAMTAGTKYKQFEE 283
 QY 131 KVA--DQVKG--VDLITIGDDNTAA--LAFLARN--YGLTV-- 174
 DB 284 RIVAVDEVRKHGNIILITDELITVAGAGAEPAIDNSILKRALRGITQIGATTID 343
 QY 175 -----GLPXTVD--NDVEPIKOST--GAWTAAB 198
 DB 344 YRKHEDKALERRPQKIVVHPSPVDETIELRLKKVYBEHNHNVITTEBALKAATLS 403
 QY 199 Q-----GARFPMNVVANNANPMLIVHEMGRNCGMLTATQOER 240
 DB 404 QYVHGFPLPKAIDLDEAGARVAVNTMO--PTDLMKEAELENTKLAKEQAIQOYE 461
 QY 241 K--LIDRAEMLP--LGLTRESY-----EVAHVPVPMAD-----LEAEK 278
 DB 462 KAGGLDBEKGKLERQSMQKQENKHEHQVDEBAVAVSLQGTGPSALTAESB 521
 QY 279 REEVD--KVCNITFVSEGAIVEAENQ-----AKQGEVPRDAFGHIKIDAVNP 329
 DB 522 KILKLEDTLRKV-----IGQNDATVSTICRAIRSRRTGIDKNNRPTGSF--LFLGPTGV 573
 QY 330 GK-WPEBOFA--OMIGAKXTLYQ--KSGYFARASAVDDKRLKSCADLAABGAFRREG 365
 DB 574 GKSLLAQQAIEFPGSDALIQVMSBYMEKFPATKQ-----KQSPFG 616
 QY 386 VIGHEDDNGVLAIE-----FPIKQKPFNIDTWFNSMLSEIGQPK-----GSK 432
 DB 617 YVGH-BEGGHLTQVRRRYCVAFLEIEKAP-----DIMLMLQILGGRITDSFGK 670
 QY 433 VEVSH 437
 DB 671 VDFRH 675

RESULT 13
 US-09-541-782-4
 ; Sequence 4, Application US/09541782
 ; Patent No. 6284480
 ; GENERAL INFORMATION:
 ; APPLICANT: Nislow, Corey
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Beraud, Christophe
 ; TITLE OF INVENTION: Antifungal Assay
 ; FILE REFERENCE: 1015

; CURRENT APPLICATION NUMBER: US/09/541,782
 ; CURRENT FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1038
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-09-541-782-4

Query Match 4.4%; Score 99.5; DB 3; Length 1038;
 Best Local Similarity 20.7%; Pred. No. 1.1;
 Matches 85; Conservative 65; Mismatches 160; Indels 101; Gaps 18;

QY 47 LNSAIGSLIERYTEIDPSIBIIICRGYKGLLDGSPYPTAEVRKAGVLFQSGSVIGN 106
 DB 685 LNTMOQESILQETNIQPNIDMI-----KNEVLITMRIMQKAEIM----- 724
 QY 107 SSVKLTNVKDCVR-----GLVKEGDEPQYAADQVLDGVDILHTTIGDDNTAA 157
 DB 725 -----YDCVYKXILNESPKFFNVVIEKIDIRVDFOKRYNIAENLSDISENNMKQ 777
 QY 158 ADLAFARANNGLVIGPKTVNDVFPKOSLGAWTAABGARYEMNVVANNANPMM 217
 DB 778 YLKHFPKNNHDEL--LNRHVDSTYENK-----RTNFVENFKVLDHLDENK 827
 QY 218 LIVHEMGRNCGMLTAATAOBYRKLID-----RAEWLPELGITRESYEVAHVPVEMAID 272
 DB 828 LIMEH-----LTTASAVIDQEMDLFEPKRYWENSFDLINDCSNNNEFYNSMAAT 879
 QY 273 LEAEKRLREVDKDKPCNIPVSEGAIVEAENQAGQ--BVRPDAFGHILDAVNP 331
 DB 880 IS-----QIKSTVDTSSSNESISV-----MKGQVESINALSLLK---NNTK 920
 QY 332 WFGQFAQWIGAKETL--VQSGYFARASAVNDM-----FLIKSCADLAABGAFR 383
 DB 921 -FNDQFEDLINHNNLKNINIKSISTSHITNVODIYNTIENIMKNYCN-----KG 971
 QY 384 SCVTHEDDNGVLAIEFPIKQKPFNIDTWFNSMLSEIGQKQKVE 434
 DB 972 NAT--KDEMTENILK--BIPNLKMKPFLNSINSVOSVL-SPKKAIE 1017

RESULT 14
 US-09-723-820-4
 ; Sequence 4, Application US/09723820
 ; Patent No. 6468760
 ; GENERAL INFORMATION:
 ; APPLICANT: Nislow, Corey
 ; APPLICANT: Sakowicz, Roman
 ; APPLICANT: Beraud, Christophe
 ; TITLE OF INVENTION: Antifungal Assay
 ; FILE REFERENCE: 1015
 ; CURRENT APPLICATION NUMBER: US/09/723,820
 ; CURRENT FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/541,782
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1038
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-09-723-820-4

Query Match 4.4%; Score 99.5; DB 4; Length 1038;
 Best Local Similarity 20.7%; Pred. No. 1.1;
 Matches 85; Conservative 65; Mismatches 160; Indels 101; Gaps 18;

QY 47 LNSAIGSLIERYTEIDPSIBIIICRGYKGLLDGSPYPTAEVRKAGVLFQSGSVIGN 106
 DB 685 LNTMOQESILQETNIQPNIDMI-----KNEVLITMRIMQKAEIM----- 724

QY 107 SRVKLTNVKDCVKR-----GLVKEGEDPQKVAADQLVKDVILHTIGDDDTNPA 157
 DB 725 -----YKDCVKKILNESPKEFNVIIEKIDILIRVDFQFKYKNIJAENLSDISENNMKQ 777
 QY 158 ADLAAFLARNYGLVLGPTVNDVFPFKOSLGAWTAAGQARYFNVAENANPRM 217
 DB 778 YLKNHFFPNKHQEL-----LNRHVDSTYENIEK-----RTNEFVENFKVLNDHLENKK 827
 QY 218 LIVHEWGRNGCWLTAATAOEYKLLD-----RAEMLELGUTRESEVEHAFVPEMAID 272
 DB 828 LHMN-----LFTATSAVIDQEMDLFBEPKRYWENSFLINDCSMNNEFYNSMAAT 879
 QY 273 LEAEAKRREVMKDCVNIFVSEGAIVEAENQAGQ-EVRDPAFGHKLDAVNPCK 331
 DB 880 LS-----QIKSTVDTSNSNNEISV-----MRQVEBSENAISILK-----NNTX 920
 QY 332 WFGQFAQMGAEKTL-----VOKSGYFARASASNVDM-----RLIKSCADLAVECAFPRE 383
 DB 921 -FNDQFQOLNKNHNLKXNKSISTSHITNDVINTENTENIMKNYGN-----KE 971
 QY 384 SGVIGHDEDMGNVLAIEPPRIKSGKPPNIDTWMENMLSEIGOPKSGKVE 434
 DB 972 NAT--KDEWIENILK--EIPMLSKMPLRLSNINSNSVOSVI--SPKKAIR 1017

RESULT 15

US-09-328-352-6730
 ; Sequence 6730, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328, 352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 6730
 ; LENGTH: 863
 ; TYPE: PR
 ; ORGANISM: Acinetobacter baumannii
 ; US-09-328-352-6730

Query Match 4.2%; Score 96; DB 4; Length 863;
 Best Local Similarity 20.9%; Pred. No. 1.8;
 Matches 104; Conservative 69; Mismatches 157; Indels 168; Gaps 26;

QY 27 TLANKPKVAIL-TNGLIAPCLNSAI-GSLERTYEIDPSIETICRGYKGLLDGSP 84
 DB 41 TLLEPSPNISLQAGARLPKQLKQALDAPFIANPTGDVNLPEAVPALNADRVA 100
 QY 85 V-----TAVRKKAGVLQRPQSVIGNSRVKLTNVKDCVKRGLVKEGEDP 129
 DB 101 QKAGBFLSTBWVLGLALETGETKNIL-----SANGVTPLSLRYTENI-RGSDKMSNN 154
 QY 130 QKVAADQLVKQGVILH-----TIGSDPTNTAADLAFLARN-----YGLT 172
 DB 155 HEDQDSINIKYITIDTERALSGKLDPIVIGRDEIRRTIOVLSRTKXNPVLIGEPGKXT 214
 QY 173 VI--GLPKTVNDVFP-----IKOSIGAMTAAGQARY-----PMNVVAENN 212
 DB 215 AIVSGIAQRIYGEVPEGLKRVKVLSDLSULA--GAKYRGFEFERLKAVALKDLAHE 271
 QY 213 ANPRMLI--VHEWGRNGC-----WLTAAATAOEYKLLDRAEWL- 249
 DB 272 GIIILFIDELHTLVAGKQDGMADGNMLKPALANGELRCGACTLDEYQYIERKDALE 331
 QY 250 -----PELGLT-----RESYEVH-----AVF-----VPEMA 270
 DB 332 RRFQKVLVDEPSEVEDTIALRGIKERKVAHGVQILDSALITAAAMSHRYITTDQLDPKA 391
 QY 271 IDL--EAEAKRLR-----EVMKVD-----CVNIFVSEGAIVEAENQAGQOE 313

DB 392 IDLIDEAASRIKWEIDSKPEALDKLDRLLIQLMQLEAVKQDSDASRAEVTLEKQIAE 451
 QY 314 VPDPAFGHKLDAVNPCKMFGSQFAQMGAEKTLVOKSGYFARASASNVDMRLIKSCA- 372
 DB 452 VEKE--YNDLEEV-----KAEKTLVSGT-----KQAVYELDKARIAPEKAQ 491
 QY 373 ---DLAVECAFPRESGVT 387
 DB 492 REGDLAE--AARLOYGVI 507

Search completed: January 29, 2004, 14:39:01
 Job time : 23 secs

RESULT 2
AC2836
hypothetical protein pfp [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C/Species: *Agrobacterium tumefaciens*
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 14-Apr-2003
C/Accession: AC2836
R/Mod: D.W.; Seubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Mo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McCell
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AC2836
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-479 <KUR>
A/Cross-references: GB:AE008688; PIDN:AL43105.1; PID:G17740576; GSPDB:GN00186
A/Experimental source: Strain C58 (Dupont)
C/Genetics:
A/Map position: circular chromosome
C/Superfamily: pyrophosphate dependent phosphofructokinase; 6-phosphofructokinase 1 hom

Query Match 56.6%; Score 1292.5; DB 2; Length 479;
Best Local Similarity 57.9%; Pred. No. 1.8e-84;
Matches 246; Conservative 71; Mismatches 101; Indels 7; Gaps 2;

QY 8 HLTADL-----RCHMFPLNPNFYTLNKKKRAIITAGGLAFLNSAIGSLIEREYIDP 63
DB HLTAAVASICQCTLWYAK--RRAMAKQKVAMLTGGALPCLSSAVGGLIERYSIDAP 110
QY 64 SIEIICRGYKGLLDGDSYPTAEVRKKAGVLOFGSGVIGNSRVKLTNNVDCVRKGLV 123
DB EIDIIVRSYGCVLLGERIEITKMRKAHLHRYGSGPIGNSRVKLTNNAADCAKGLV 170
QY 124 KEGEDPQKVAADQVYKQVDIITHTGGDPTNTAAADLAFLARNNGYLVIGLPTVDND 183
DB KEGNPLRVAERLADPDIITHTGGDPTNTAAADLAFLARNNGYLVIGLPTVDND 230
QY 171 KEGNPLRVAERLADPDIITHTGGDPTNTAAADLAFLARNNGYLVIGLPTVDND 230
QY 184 VEPITKOSLGANTAAEQGARYFMNVVAENANPRMLIVHEWGRNGCMITAAAOEYKLL 243
DB VEPITKOSLGANTAAEQGARYFMNVVAENANPRMLIVHEWGRNGCMITAAAOEYKLL 290
QY 231 VEPITKOSLGANTAAEQGARYFMNVVAENANPRMLIVHEWGRNGCMITAAAOEYKLL 290
QY 244 DRAEWLPELGLTRBSYEVHNAVPEMAIDLEAERKLEWMDKVCNIFVSEGAVEAI 303
DB KNDYVBGLMMNTQKNIIDGILPEMAFDLEAERKLEWMDKVCNIFVSEGAVEAI 350
QY 304 VAEQAKQGVPRDPAFGHIKLDVAVNPKFGEQPAQMI GAETLVQKSGYFARASASND 363
DB VAEQAKQGVPRDPAFGHIKLDVAVNPKFGEQPAQMI GAETLVQKSGYFARASASND 410
QY 351 VAEQAKQGVPRDPAFGHIKLDVAVNPKFGEQPAQMI GAETLVQKSGYFARASASND 410
QY 364 DMLIKSCADLAVECAPRESGVIGHEDNGNVLRAIEPRPIKSGRPNIDTDFENMLS 423
DB DMLIKSCADLAVECAPRESGVIGHEDNGNVLRAIEPRPIKSGRPNIDTDFENMLS 470
QY 424 EIGQP 428
DB 471 HWGP 475

RESULT 3
P97613
pfi-phosphofructokinase (AF246209) [imported] - *Agrobacterium tumefaciens* (strain C58, C
C/Species: *Agrobacterium tumefaciens*
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 14-Apr-2003
C/Accession: P97613
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirillo, B.; Goldman,
A.; Liu, F.; Mollan, C.; Allinger, M.; Doughty, D.; Scott, C.; Dapkas, C.; Markez, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: P97613
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-514 <KUR>
A/Cross-references: GB:AE007669; PIDN:AAK8763.1; PID:G15157249; GSPDB:GN00186
A/Genetics:
A/Map position: circular chromosome

Query Match 56.6%; Score 1292.5; DB 2; Length 514;
Best Local Similarity 57.9%; Pred. No. 2e-84;
Matches 246; Conservative 71; Mismatches 101; Indels 7; Gaps 2;

QY 8 HLTADL-----RCHMFPLNPNFYTLNKKKRAIITAGGLAFLNSAIGSLIEREYIDP 63
DB HLTAAVASICQCTLWYAK--RRAMAKQKVAMLTGGALPCLSSAVGGLIERYSIDAP 145
QY 64 SIEIICRGYKGLLDGDSYPTAEVRKKAGVLOFGSGVIGNSRVKLTNNVDCVRKGLV 123
DB EIDIIVRSYGCVLLGERIEITKMRKAHLHRYGSGPIGNSRVKLTNNAADCAKGLV 205
QY 124 KEGEDPQKVAADQVYKQVDIITHTGGDPTNTAAADLAFLARNNGYLVIGLPTVDND 183
DB KEGNPLRVAERLADPDIITHTGGDPTNTAAADLAFLARNNGYLVIGLPTVDND 265
QY 184 VEPITKOSLGANTAAEQGARYFMNVVAENANPRMLIVHEWGRNGCMITAAAOEYKLL 243
DB VEPITKOSLGANTAAEQGARYFMNVVAENANPRMLIVHEWGRNGCMITAAAOEYKLL 325
QY 244 DRAEWLPELGLTRBSYEVHNAVPEMAIDLEAERKLEWMDKVCNIFVSEGAVEAI 303
DB KNDYVBGLMMNTQKNIIDGILPEMAFDLEAERKLEWMDKVCNIFVSEGAVEAI 385
QY 304 VAEQAKQGVPRDPAFGHIKLDVAVNPKFGEQPAQMI GAETLVQKSGYFARASASND 363
DB VAEQAKQGVPRDPAFGHIKLDVAVNPKFGEQPAQMI GAETLVQKSGYFARASASND 445
QY 386 VAEQAKQGVPRDPAFGHIKLDVAVNPKFGEQPAQMI GAETLVQKSGYFARASASND 445
QY 446 DMLIKSCADLAVECAPRESGVIGHEDNGNVLRAIEPRPIKSGRPNIDTDFENMLS 423
DB DMLIKSCADLAVECAPRESGVIGHEDNGNVLRAIEPRPIKSGRPNIDTDFENMLS 505
QY 424 EIGQP 428
DB 506 HWGP 510

RESULT 4
T35500
6-phosphofructokinase (BC 2.7.1.11) - *Streptomyces coelicolor*
C/Species: *Streptomyces coelicolor*
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 12-May-2003
C/Accession: T35500; T42063
R/Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z21580
A/Accession: T35500
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-342 <SEB>
A/Cross-references: EMBL:AL09661; PIDN:CA851967.1; GSPDB:GN00070; SCODEB:SCGE10.13C
A/Experimental source: strain A3(2)
R/Alves, A.M.; Ruvierink, G.J.; Bibb, M.J.; Dijkhuizen, L.
Appl. Environ. Microbiol. 63, 956-961, 1997
A/Title: Identification of ATP-dependent phosphofructokinase as a regulatory step in the
A/Reference number: Z22050; MUID:97208211; PMID:9055413
A/Accession: T42063
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-342 <ALV>
A/Cross-references: EMBL:U51728; NID:G1931572; PIDN:AAK45135.1; PID:G1931573
C/Genetics:
A/Map position: circular chromosome
C/Superfamily: 6-phosphofructokinase, bacterial type; 6-phosphofructokinase 1 homology

C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 13.6%; Score 311; DB 2; Length 342;

Best Local Similarity 27.4%; Pred. No. 1e-14;

Matches 105; Conservative 63; Mismatches 137; Indels 78; Gaps 17;

34 KVALITAGGLAPCLNSAIGSLERYTEIDPSEIICRGYKGLLGDSPYTAAYARKA 93

2 KQVGLVGGGDCPEGLMNVIRAVKGVQ-EKGYDFGFRGMRGPLEGDTVPL--DIPAR 58

94 GVLQRFSGSVIGNSRYKLTNVKDCVKRGVKEGSDPQKVAADQVKGVDLIHTTGDDT 153

59 GLIPR-GGVYIGSSSRNPVKORDIR-----IKMTALGVEALITIGGSDT 105

154 NFAAADLAFIAANNGLTVIGLPTVNDVFPKQSLGAMTAAGGARYFNNVAENNA 213

106 LGVATLDA-----DEGVPCVGPVKITIDLSATDTPGDTAVGATATAIDRLHTTAS 160

214 NPMRLIVHEVMGRNCGMLTAAATQAEYRKLLDRAEMLPBGLTRBSYEVAHVPEMAIDL 273

161 HEMLVV-EVMGRHAGMIALHS-----GLAGGA---NVILIPGQFVDV 199

274 EA-----EAPRLRVDKDCVNI FVSEGAQVEAIVAEQAKGQVPR---DAFGHIKD 325

200 EGVCSWTSRFRASVAPL-----VVVAEGA-----MRDDDMVLKDSLDSTYGHVRLS 247

326 AVNPGKMPGEQFQMIKGA-KTLVQSGYFAPASASNVDPMLIKSCADLAVECAFRRES 384

248 GV--GEMLAKQIEKRTGNERTTV--LGVQKGTSPASAPRLATRFGLHAYDCV----- 298

385 GVIGHDEDNQNT--LRAIEFPRI 405

299 ---HDGDFGMVAFRGTDIVRV 317

RESULT 5

PRO190

probable diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) - Lyme dise

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 14-Apr-2003

C:Accession: F70190

R:Reaser, C.M.; Casrens, S.; Huang, M.M.; Sutnon, G.G.; Clayton, R.; Lachigra, R.; White

son, D.; Peterson, J.; Krelavge, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943; PMID:9403685

A:Accession: F70190

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-448 <LDB>

A:Cross-references: GB:AE001172; GB:AE000783; NID:g268654; PIDN:AA67070.1; PID:g26865

A:Experimental source: strain B31

C:Superfamily: pyrophosphate dependent phosphofructokinase; 6-phosphofructokinase 1 homo

C:Keywords: phosphotransferase

F:82-398/Domain: 6-phosphofructokinase 1 homology <6PF>

Query Match 11.8%; Score 270; DB 1; Length 448;

Best Local Similarity 24.9%; Pred. No. 1.3e-11;

Matches 102; Conservative 69; Mismatches 177; Indels 62; Gaps 11;

34 KVALITAGGLAPCLNSAIGSLERYTEIDPSEIICRGYKGLLGDSPYTAAYARKA 93

81 KALITTCGGLCPGFNDVIRISIVTLTKYGVNIVGVKFGYGLLPESNSPININPDV 140

94 GVLQRFSGSVIGNSRYKLTNVKDCVKRGVKEGSDPQKVAADQVKGVDLIHTTGDDT 153

141 DDINKFGGIIIGSS-----RGKIKVE-----IVTLERMINIMENIGGGT 183

154 NFAAADLAFIAANNGLTVIGLPTVNDVFPKQSLGAMTAAGGARYFNNVAENNA 213

184 QKGSLLIAEIERKMLIKIAVVGIPKTVNDFMFVQKSGFETAVQAAVAAGAFREANS 243

214 NPMRLIVHEVMGRNCGMLTAAATQAEYRKLLDRAEMLPBGLTRBSYEVAHVPEMAIDL 273

244 AVNGLVAVKVMGRDGGFIAAHTA-----LSNDVNFCLIPEDPDI 284

274 EAE-----AKEL--REVMQKDCVNI FVSEGAQVEAIVAEQAKGQVPR---RDAFGHI 322

285 EGNPGFVHLERRLLEKSLSEBIPHAVALILABAG-----QYFDFHFKKODSGTL 336

323 KLDVNPCKMGEQFQMIKGAEK--TLVQ-KSGYFAPASASNVDPMLIKSCADLAVEC 378

337 LYEDI--GLYIKDKITTEYFAKNIQFTLYIDPSYILIRSSPANADSDLYCARLSNAVA 394

379 AFRESGVIGHDEDNQNT--LRAIEFPRIKGPENIDTQMSMSEIQP 428

395 KMAKTKMLISLWSTKVFVHTIPKNAVIDRKN-VNPNSGFMVDVASTGP 443

RESULT 6

S49458

diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) (validated) - Entamo

C:Species: Entamoeba histolytica

C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 14-Apr-2003

C:Accession: S49458; S68243; S52082

R:Bruchhaus, I.

submitted to the EMBL Data Library, October 1994

A:Reference number: S49458

A:Accession: S49458

A:Molecule type: mRNA

A:Residues: 1-436 <BRN>

A:Cross-references: EMBL:X82173; NID:G558573; PIDN:CAAS7659.1; PID:G558574

R:Bruchhaus, I.; Jacobs, T.; Denart, M.; Tannich, B.

Biochem. J. 316, 57-63, 1996

A>Title: Pyrophosphate-dependent phosphofructokinase of Entamoeba histolytica: molecular

A:Reference number: S68243; MUID:96235172; PMID:8645233

A:Accession: S68243

A:Molecule type: mRNA

A:Residues: 1-429, 'T', 431-436 <BRU>

A:Cross-references: EMBL:X82173; NID:G558573

A>Note: the authors present evidence of the enzymes activity

A:Note: the sequence is revised in Genbank entry EHPRIFFX, release 114, (PIDN:CAAS7659.1

R:Huang, M.; Albach, R.A.; Chang, K.P.; Tripathi, R.L.; Kemp, R.G.

Biochim. Biophys. Acta 1260, 215-217, 1995

A>Title: Cloning and sequencing a putative pyrophosphate-dependent phosphofructokinase g

A:Reference number: S52082; MUID:95143279; PMID:7841199

A:Accession: S52082

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 46-108, 'R', 110-416, 'NEIT', 435, 'MDHYLL', <HDA>

A:Cross-references: EMBL:U12513; NID:G529008; PIDN:AAA92671.1; PID:G529009

C:Genetics:

A:Gene: Eh/PEP1-PFK

C:Superfamily: pyrophosphate dependent phosphofructokinase; 6-phosphofructokinase 1 homo

C:Keywords: phosphotransferase

Query Match 11.5%; Score 263.5; DB 1; Length 436;

Best Local Similarity 26.3%; Pred. No. 3.5e-11;

Matches 108; Conservative 68; Mismatches 164; Indels 71; Gaps 16;

34 KVALITAGGLAPCLNSAIGSLERYTEIDPSEIICRGYKGLLGDSPYTAAYARKA 91

82 KVALITTCGGLCPGLMNVIRISIVTLTKYGVNIVGVKFGYGLLPESNSPININPDV 139

140 -VSDIHQKGGIIIGTSR-----GAQSPVMAQFLIDNNFNIIFFTGSD 181

152 DYNFAADLAFIAANNGLTVIGLPTVNDVFPKQSLGAMTAAGGARYFNNVAEN 211

182 GTERGAATANKELERRKVPITVVGIPKTVNDICTYDSTGFQTAVGLSQEATRAVHSEA 241

212 NPMRLIVHEVMGRNCGMLTAAATQAEYRKLLDRAEMLPBGLTRBSYEVAHVPEMAI 271

Db 242 KSANNGIGVRLWGRDGRGFTAL-----YASLANG-----DANVLIPEDID 282

Qy 272 DL-----SAAKRLREVMADKYDCVNI FVSEAGAVEAIVAEKQGEVPRDAFGI-KLDA 326

Db 283 PIQIGCFVQKR---INSGHV-IVABGA-----LQNKRPDLDLGDTKSNILHMS 333

Qy 327 VNRKMGGEQPAQMTGAEKLVQ--KSGYFARASAVNDKRLIKSCADLAVECAPRRRS 384

Db 334 INVLRSITLYKSLIGIEHTIYFVDPSTYIRAPCSAAAHPCMKLANAAVAVAGKTI 393

Qy 385 G-VIGHEDGNVYLRALIEPRP---IKGKPFNIDTDV-FNSMSEIGQPK 429

Db 394 GLVICHNNH---FVSYPIRDTSTYIK-----RVNIDGPLYTMSAIERK 436

RESULT 7

T06011
probable diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) T25K17.80
N:Alternate names: protein T25K17.80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 14-Apr-2003
C:Accession: T06011
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15382
A:Accession: T06011
A:Molecule type: DNA
A:Residues: 1-500 <BEV>
A:Cross-references: EMBL:AL049171; GSPDB:GN00062; ATSP:T25K17.80
A:Experimental source: cultivar Columbia; BAC clone T25K17
C:Genetics:
A:Gene: ATSP:T25K17.80
A:Map position: 4
A:introns: 46/2; 59/3; 80/3; 141/3; 194/3; 212/3; 235/3; 279/1; 367/3; 383/1; 434/3
C:Superfamily: pyrophosphate dependent phosphofructokinase; 6-phosphofructokinase 1 homoc
C:Keywords: phosphotransferase

Query Match 11.3%; Score 257.5; DB 2; Length 500;
Best local similarity 25.6%; Pred. No. 1,1e-10;
Matches 109; Conservative 59; Mismatches 167; Indels 91; Gaps 16;

Qy 37 ILTAGGLAPCLNSAIGSL-----IERYTEIDPSIELIC-----YRGYKGL 78

Db 92 IYVCGGCLPGLNTYIRIVASLSYMGVKKILDIVS---FCDNMLLTNTNGGYRGY 148

Qy 79 LGSYPTAARVKKAGVLRGFGSVIGNSRVKLTNVDCYKGLVKGSDPOKVAADQV 138

Db 149 AKNTVSDSV---VNDIHRGGTILGTSR-----GHDTTKI-VDSIQ 188

Qy 139 KDGVDILHTIGDDTNTAAADLAFLANNYGLTVIGLPETVDNVFPIKQSIGAWTAAE 198

Db 189 DRGNGVYIIGDGTGAGAVIFEEIRRGKLVAVIGIPIKTDNDIPVIDKSGFDPAVE 248

Qy 199 QGARFVNVVAENRANPRMLTYHEWGRNGMLTAATAGYRKLDRAEMLPELGITRES 258

Db 249 EAORAINAAHVESIESIENGIGYKMGKRGYSGLA-----KYATLAS 289

Qy 259 YEYAAVFPVPMALDLEAA-----KRLREVMADKYDCVNI FVSEAGAVEAIVAEKQAG 311

Db 290 RDVDCCLIPSPFLYBEGGLFYIERKLKESGHV---LVIAKGGQDLMKSMESM- 344

Qy 312 QEVPRAFGIHKLDANNPKGWFGEQPAQMTGAETLVQ---KSGYFARASASVNDMEL 367

Db 345 --TLKASGKMLKDV--GLMLOSIKDHFNRKMMVNTKYIDPTMIRVPSNASDNY 400

Qy 368 IKSCADLAVECAPRREGVIGHEDGNV---LRATIEPRIKGKPFNIDTDV-FNSM 422

Db 401 CTLLAGSAHGAAGAGTYGI-----SGLVNGRQTYIPFYITKQKHVVITDMAR-LL 454

Qy 423 SETGQP 428

Db 455 SSTNQP 460

RESULT 8

C72406
6-phosphofructokinase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 12-May-2003
C:Accession: C72406
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sex
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72406
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <ARN>
A:Cross-references: GB:AE001705; GB:AE000512; NID:g4980694; PIDN:AA035301.1; PID:g498071
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0209
C:Superfamily: 6-phosphofructokinase, bacterial type; 6-phosphofructokinase 1 homology
F:4-279/Domain: 6-phosphofructokinase 1 homology <6FF>

Query Match 11.1%; Score 253; DB 2; Length 319;
Best local similarity 26.6%; Pred. No. 1.3e-10;
Matches 95; Conservative 60; Mismatches 126; Indels 76; Gaps 14;

Qy 33 KKVAILTAGGLAPCLNSAIGSLIERYTEIDPSIELICYRGYKGLLDSDYPTAEVRK 92

Db 2 KRIAVITSGDAFGNAAVAVV-RY-GVRCGLVYIGVRGSGIIDGPF--VKLEYKDV 57

Qy 93 AGVLRFGSVIGNSRVKLTNVCKVKGGLVKEGSDPOKVAADQVVKGVDLHTIGSD 152

Db 58 AKITK-GGTLIRTCRCEPFT-----REGSLAKQCKKKGISGLVIGSG 104

Qy 153 TMTAAADLAFLANNYGLTVIGLPETVDNVFPIKQSIGAWTAAEGARFVNVVAENN 212

Db 105 SLT-----GAILLYEHNKIPVGIPIATIDNDIGLDMCIGVDTCLNTWDAVQKLDRTAS 159

Qy 213 ANPKLTYHEWGRNGMLTAATAGYRKLDRAEMLPELGITRESYEVHAFVPEMAD 272

Db 160 SHERAFIV-EWGRSGYIALMAG---LVYGA-----ALIVEIIPVD 198

Qy 273 LEAEKRLREV--MDKDCVNI FVSEAGAVEAIVAEKQGEVPRDAFGHKLDANNPG 330

Db 199 YSQLDRILIEERRKINSI-IIYVAGASAVTAR-----HLE----- 236

Qy 331 KWFGEQPAQMTGAETLVQKSGYFARASASVNDMELIKSCADLAVECAPRREGV 387

Db 237 -----YRIGYE-TRITIIHVGQSGPTAFDRRLASMGVAVADLLDGEVDVM 284

RESULT 9

T13433
pyrophosphate-dependent phosphofructo-1-kinase homolog T13433.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 14-Apr-2003
C:Accession: T13433
R:Bevan, M.; Leonard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, July 1999
A:Reference number: Z17683
A:Accession: T13433
A:Molecule type: DNA
A:Residues: 1-473 <BEV>
A:Cross-references: EMBL:AL096692; GSPDB:GN00062; ATSP:T13433.40
A:Experimental source: cultivar Columbia; BAC clone T13433
C:Genetics:
A:Gene: ATSP:T13433.40
A:Map position: 4
A:introns: 35/3; 51/2; 64/3; 85/3; 131/3; 202/3; 225/3; 269/1; 358/3; 373/1; 424/3
C:Superfamily: pyrophosphate dependent phosphofructokinase; 6-phosphofructokinase 1 homoc

F:95-405/Domain: 6-phosphofructokinase 1 homology <6PF>

Query Match

Best Local Similarity 11.0%; Score 251; DB 2; Length 473;
Pred. No. 3,1e-10;
Matches 103; Conservative 60; Mismatches 174; Indels 72; Gaps 15;

```

QY 37 ILTAGGLAECGSLIERTETDPSRIICRYGSGLLGDSVPYARKKAGVL 96
DB 97 IYVCGGLCEPLAVHIEICGLSYMGVKKILIDIGTGKFAKRTIHDL--KTVNDI 153
QY 97 QRFSGVIGNSRVKLTNNVXDCVKGESDPQKVAADQLVGDVLLHTIGDDPTNVA 156
DB 154 HESGGLTIGTSR-----GSHNTTKI-VDSIQRGINGVYIIIGDSSQSG 196
QY 157 AADLAFPLARNTKGLTVIGLPTVDVDVPEPIKSLGAMTAEGCAEYEMVVAENANR 216
DB 197 AAFIEIRKRLKLVAVAGIPKTIIDIPILDSFDPDAVEBQAIINAAHEATSPEN 256
QY 217 MLIVHEVMGNCMLTAATAGVYKLDLBAEWLPELGLTRESYEVHAFVPEMAIDLEAR 276
DB 257 GIGLVLMGRYSGFIA-----MHATLASRDVDCCLIPSPFLBGS 297
QY 277 A-----YREHWDKVDCCNIFVSESGAVEATVAEQAKQOEVRDAFGHIKLDVAVNP 329
DB 298 GGLFEFIDRLKSKSHNV-----IVIAEGAGQDLSESM--KESTTLKDSGKMLQDI-- 349
QY 330 GWFEGQAPQMGAEKTLVQK---SGYFARASASNVDMRLKSCADLAVECAFRESGV 386
DB 350 GLWISORIKDHAKKQTLTLKTYIDPTMYLRAPDSNSD---NVCTTLAQSVAH---GV 402
QY 387 I-GHDEDNQVLA---IEFPII-KGQKFPNIDPTMNSLSEIGCP 448
DB 403 MAGYNGFTVGLVNGRHTYIPENRITKOKKXVITDGMAR-LLSTNQP 450

```

RESULT 10

J00016 6-phosphofructokinase (EC 2.7.1.11) alpha chain - yeast (Saccharomyces cerevisiae)

N.Altternate names: phosphofructokinase 1; phosphohexokinase; protein 194; protein G8599;
C.Species: Saccharomyces cerevisiae

C.Date: 31-Mar-1990 #sequence revision 14-Jul-1999 #ext change 12-May-2003
C.Accession: J00016; S38963; S57708; S64566; S64564; S63924

R.Helmsch, U.; Ritzel, R.G.; von Borstel, R.C.; Aguilera, A.; Rodicio, R.; Zimmermann,
Gene 78, 309-321, 1989

A.Title: The phosphofructokinase genes of yeast evolved from two duplication events.
A.Reference number: A91608; MUID:89378757; PMID:2528496

A.Accession: J00016

A.Molecule type: DNA

A.Residues: 1-987 <HEI>

A.Cross-references: EMBL:M26943; NID:g172137; PIDN:AAA34859.1; PID:g172138

R.Koperechlaeger, G.; Baer, J.; Stelwagen, E.
Eur. J. Biochem. 217, 527-533, 1993

A.Title: Limited proteolysis of yeast phosphofructokinase. Sequence locations of cleavage
A.Reference number: S38963; MUID:94039086; PMID:8223596

A.Accession: S38963

A.Molecule type: Protein

A.Residues: 1-6,90-97,197-205,914-921 <KOP>

R.van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.
submitted to the EMBL Data Library, June 1995

A.Description: Sequence analysis of the 43 KB CRM1-YIM9-PTS4-SMII-PHO81-YHB4-PFK1 region
A.Reference number: S57708

A.Accession: S57708

A.Molecule type: DNA

A.Residues: 794-987 <VAN>

A.Cross-references: EMBL:X87941; NID:g886908; PIDN:CAA61193.1; PID:g886937

A.Experimental source: strain S288C
R.Guerreiro, P.; Barreiro, T.; Azevedo, D.; Rodrigues-Pousada, C.
submitted to the Protein Sequence Database, May 1996

A.Reference number: S64565

A.Accession: S64566

A.Molecule type: DNA

A.Residues: 1-987 <GUB>

A.Cross-references: EMBL:Z73025; NID:g1323434; PIDN:CAA97268.1; PID:g1323435; GSPDB:GN00

A.Experimental source: strain S288C

R.van der Aart, Q.J.M.; Steensma, H.Y.

submitted to the Protein Sequence Database, May 1996

A.Reference number: S64541

A.Accession: S64564

A.Molecule type: DNA

A.Residues: 794-987 <VAN>

A.Cross-references: EMBL:Z73025; GSPDB:GN00007; MIPS:YGR240C

A.Experimental source: strain S288C

R.van der Aart, Q.J.M.; Kleine, K.; Steensma, H.Y.
Yeast 12, 385-390, 1996

A.Title: Sequence analysis of the 43 kb CRM1-YIM9-PTS4-DIR2-SMII-PHO81-YHB4-PFK1 region
A.Reference number: S63896; MUID:96267763; PMID:8701610

A.Accession: S63924

A.Molecule type: DNA

A>Status: nucleic acid sequence not shown; translation not shown

A.Residues: 794-987 <VAF>

A.Cross-references: EMBL:X87941; NID:g886908; PIDN:CAA61193.1; PID:g886937

A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

C.Comment: Phosphofructokinase is composed of four alpha chains and four beta chains.

C.Genetics:

A.Gene: SGD:PFK1; MIPS:YGR240C

A.Cross-references: SGD:S0003472; MIPS:YGR240C

A.Map position: 7R

C.Superfamily: 6-phosphofructokinase, eukaryotic type; 6-phosphofructokinase 1 homology

F:208-517/Domain: 6-phosphofructokinase 1 homology <6PF1>

F:596-886/Domain: 6-phosphofructokinase 1 homology <6PF2>

F:1225-1229/Binding site: AMP, allosteric (Arg) #status predicted

F:309-310/Binding site: ATP (Asp, Gly) #status predicted

F:356/Active site: Asp #status predicted

F:398-455,482-488,491-729/Binding site: fructose-6-phosphate (Met, Glu, Lys, His, Arg, C

F:751/Binding site: citrate, allosteric (Lys) #status predicted

Query Match

10.8%; Score 246.5; DB 1; Length 987;
Best Local Similarity 23.9%; Pred. No. 1,8e-09;
Matches 103; Conservative 68; Mismatches 135; Indels 125; Gaps 19;

```

QY 31 KPKVAVITAGGLAECGSLIERTETDPSRIICRYGSGLLGDSVPYARKKAGVL 90
DB 204 KKKKIAVNTSGDSDGMMAVRAVVR--TGHPGQDFAVYBEGGLRGCKT-----LK 256
QY 91 KKA-----GVLQRFSGSVIGNSRVKLTNNVXDCVKGELVGEDEPQKVAADQLVGDVDT 145
DB 257 KMAVEDVAGMUSE--CGTLIGTA-----RSMFRREBRBQQAAGMLISQIDAL 303
QY 146 HTIGGDDPTNVAADL-----AFLARNTY-----GLTVIGLPTVNDVPEPI 187
DB 304 VVCGGDSGLT--GAULPHEHWPDLVDLVAEGRFKEEVAAPYKRLSTVGLVGSINDMSGT 362
QY 188 KQSLGAMTAABOGARYEMNVVAENANPRLILVERWGRNCMTL-----ATAOEYRKL 243
DB 363 DSTIGAVSALERICEMVDYIDATKSHSRAPV--EVWGRHCGMLAAMAGIATGADY----- 417
QY 244 DRAEMLPELGLTRESYEVHAFVPEMAIDLEAERKILREVMQKDCV-----NIFVSEGA 298
DB 418 -----IFIPERAVPFGKMODELKEVOCORRSKGRNNITIVAEGA 457
QY 299 -----GVEATVAEQAKQOEVRDAFGHIK--DAVNGSKMFGEGEPAMIGAEK 345
DB 458 LDDQANVTYANDVADALIEL-----GLDYKVTILGHVQGGGAVVAHDRLAT--LOGVDAYK 512
QY 346 TLVQKSGYFAPASASN-----VDDMLIKSCADLAVECAFRESGVIGHDE 391
DB 513 AYVE-----FTPEPSPILIGILENKIRIMPLVESYKLTLSVA-----TAIENKDF 557
QY 392 DNGNVLTAIEF 402
DB 558 DKALSLDTEF 568

```

RESULT 11

S32902

QY 83 YPVTAEVRKAGVLAGRFSGVIGNSRVKLTNVADCVKRGVKEGEDPOKVAADQVYKQV 142
 DB 66 SKVEITLDSVSRHIEGGSLIKTSRANP-----KQEPLOQV-VKQLOKQEV 113
 QY 143 DILHTTGDDTNTAAADLAFLARNYGLTVGLPCTVDNDVFPRIKQSL--GAMTAEQ 199
 DB 114 SILVTIGGDD--TAFSSMSVAKAANN-ELHVCVPTINDL-PLVYGLPTGYEARAF 169
 QY 200 GARFENNVAAENNANRKLIVHEVNGRNGMLT--AAAPQERKLLDAEWLPELGLTR 256
 DB 170 GAVVENVLNTDASTASRYFTV-VAMGRQGHLAGIGKAGSHLTLPB-EZLP-----TT 223
 QY 257 ESEYVAVF--VPEMAIDPEAS-AKRLREVMKVDQVNIFFSESGAGVAVIEM-QAKGQ 312
 DB 224 DSEPEVTSRICDM--TEASTIKRL--YTSKKGHVIVLEGLLETVSTBELKQAFS 278
 QY 313 EYPRDAFGHITKLDVAVNGKWFGEQFAQMT--GAETLVOKS-GYPARASASVNDMLLI 368
 DB 279 SLKYDADHIMIAELDFGLVDEMEERMRRLKIAFERKMGYELFACAPNAPFREYV 338
 QY 369 KSCADLAECAPRRESGVIGHEDNGNVLRALIEPRIKGK--PRNIDTDMNSLSEIG 426
 DB 333 RDLGNARVYLLANGNGAL-----ITVGKRVPLSPD-----DLK 374
 QY 427 QPKGK-----YEVS 436
 DB 375 DPKTKTRTROYDVS 389

RESULT 14

AH0942
 6-phosphofructokinase [imported] - Salmonella enterica subsp. enterica serovar Typhi (str. Typhimurium) [NCBI]
 A:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: This species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-May-2003
 C:Accession: AH0942
 R:Parthill, U.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, M.; T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Mould, S.; O'Gaora, P.
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Nature 413, 848-852, 2001
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
 A:Reference number: AB0502; MIMD:21534947; PMID:11677608
 A:Accession: AH0942
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-320 <PAR>
 A:Cross-references: GB:AF513382; PIDN:CAD09562.1; PID:g16504676; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3809
 C:Superfamily: 6-phosphofructokinase, bacterial type; 6-phosphofructokinase 1 homology

Query Match 10.5%; Score 240.5; DB 2; Length 320;
 Best Local Similarity 24.8%; Pred. No. 1e-09;
 Matches 102; Conservative 59; Mismatches 122; Indels 129; Gaps 18;
 QY 33 KKVAILTAGGLAPCLNSAIGSLIERYTEIDPSIICRYGKYGL-----LLGDSYPTVA 87
 DB 3 KKIIGVLTSGDAPGMAAIGRVV--AAITGGLVEMGIYDGLYEDRWVQLDRYSVD 60
 QY 88 EVRKAGVLAGRFSGVIGNSRVKLTNVADCVKRGVKEGEDPOKVAADQVYKQV 147
 DB 61 MINR-----GGFPLSAR--PEPRD-----ENIRVALENKKRISIDLVV 100
 QY 148 IGGDDTNTAAADLAFLARNYGLTVGLPCTVDNDVFPRIKQSL--GAMTAEQ 207
 DB 101 IGGDSYVGAARL-----TEMGFPCIGLPCTINDIKGTDTYITGIFTALGTVEALDRL 154
 QY 208 VAENNANRKLIVHEVNGRNGMLTAAQGYRKLDAEWL--PELGLTRESYVAVF 265
 DB 155 RDTSSSHORISIV-EVMGRYCGDILLAA-----IAGCEPIVAVPEVFNRE----- 200
 QY 266 VPEMAIDPEASAK-----RLREVMKVDQVNIFFSESGAGV--AIVAEQAK 310

DB 201 -----DLVAETKAGIANGKRAIYATHEMCDVDELHAFIEKRGRETRATVLAGHIGG 254
 QY 311 QGEVPRDAFGHITKLDVAVNGKWFGEQFAQMTGAETLVOKSGYFARASASVNDMLLI 370
 DB 255 GSPFVYD-----RILASRQAV----- 272
 QY 371 CADLAVF-----CAFRRESVIGHEDNGNVLRALIEPRIKGKPRNIDTDM 417
 DB 273 -IDLILBHGGRGVGIGQNEQLVHD-----IIDALENKK-----RPFK--SDW 312

RESULT 15

KIECRA
 6-phosphofructokinase (EC 2.7.1.11) 1 - Escherichia coli (strain K-12)
 N:Alternate names: phosphofructokinase 1, isozyme 1, phosphohexokinase, isozyme 1
 C:Species: Escherichia coli
 C:Date: 31-Dec-1988 #sequence_revision 10-Oct-1997 #text_change 12-May-2003
 C:Accession: G65197; A25206; S40859
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
 A.; Rose, D.U.; Mau, B.; Shao, Y.
 A:Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MIMD:97426617; PMID:9278503
 A:Accession: G65197

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-320 <BLAT>
 A:Cross-references: GB:AE000466; GB:U00096; NID:G2367328; PIDN:AACT6898.1; PID:g1790350;
 A:Experimental source: strain K-12, substrain MG1655
 R:Hellings, H.W.; Evans, P.R.
 A:Title: Nucleotide sequence and high-level expression of the major Escherichia coli pho
 A:Reference number: A91144; MIMD:85203917; PMID:3158524
 A:Accession: A25206

A:Molecule type: DNA
 A:Residues: 1-73, 'C', 75-102, 'DG', 105-162, 'P', 164-316, 'E', 318, 'W', 320 <HELV>
 A:Cross-references: GB:X02519; NID:g42365; PIDN:CAM26356.1; PID:g42366
 A:Note: This sequence has since been corrected
 R:Evans, P.R.
 A:submitted to the EMBL Data Library, October 1986
 A:Reference number: A94501
 A:Contents: annotation; corrections
 R:Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
 A:Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from 8
 A:Reference number: S40802; MIMD:93347969; PMID:8346018
 A:Accession: S40859

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-320 <PLU>
 A:Cross-references: EMBL:LI19201; NID:g304961; PIDN:AA803048.1; PID:g305019
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1993
 C:Comment: The active enzyme catalyzes the key control step of glycolysis, the phosphory
 Y ADP and inhibited by phosphoenolpyruvate.
 C:Comment: In E. coli this enzyme is responsible for 90% of the phosphofructokinase acti
 ymes are different kinetically; there is also no immunological cross-reactivity.
 C:Genetics:
 A:Gene: pfkA

A:Map position: 88 min
 C:Superfamily: 6-phosphofructokinase, bacterial type; 6-phosphofructokinase 1 homology
 C:Keywords: allosteric regulation; ATP; glycolysis; homotetramer; phosphotransferase
 F:5-279/Domains: 6-phosphofructokinase 1 homology <6PFI>

Query Match 10.4%; Score 238.5; DB 1; Length 320;
 Best Local Similarity 24.9%; Pred. No. 1.4e-09;
 Matches 100; Conservative 65; Mismatches 132; Indels 105; Gaps 18;
 QY 33 KKVAILTAGGLAPCLNSAIGSLIERYTEIDPSIICRYGKYGL-----LLGDSYPTVA 87
 DB 3 KKIIGVLTSGDAPGMAAIGRVV--SALTGGLVEMGIYDGLYEDRWVQLDRYSVD 60
 QY 88 EVRKAGVLAGRFSGVIGNSRVKLTNVADCVKRGVKEGEDPOKVAADQVYKQV 147

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Db      61 MINR-----GGTFSSAR--FPERD-----ENIRAVAIENLKKRGIDALV 100
Qy      148 IGGDPTTAADLAFLARNNYGLTVIGLPTVDNDVEPIKOSLGAMTAAEQARYFMNV 207
Db      101 IGGDGSYMGAMRL-----TEMGFPCIGLPGTIDNDIKGTDYTIQFFTALSTVVEAIDRL 154
Qy      208 VAENNANPRMLIVHEVMGRNCGMLTAATQOEYRKLLDRAEW--LPBLGLTRESYEVAHF 265
Db      155 RDTSSSHQRIISV--EWMGRYCGDLTLAA-----LAGCEPVVVEVERRED-----L 202
Qy      266 VPEMAIDLEAEKR-----LREVMKVDVCNIFVSBGAVE---AIVEMQAKQOEYPRD 317
Db      203 VNEIKAGI-ARKGKEAIVAITHEMCDVDLAFIEKGTRETRATVGHIGGSPVPYD 261
Qy      318 AFGHIKLDAVNPCKWGEQFQMIKAETLVOKSGYFAPASASNVDMRLIKCADLAVE 377
Db      262 RI-----LASRMGAVAIDLILAGYGR----- 283
Qy      378 CAFRESGVIGHEDNGNVLRAIEPPIKGGKPPNIDTWFN 419
Db      284 CVGIONEQLVHHD-----IIDAIENMK---RPFK--GDWLD 314

```

Search completed: January 29, 2004, 14:38:27
 Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:08:27 ; Search time 17 Seconds

(without alignments)
1208.863 Million cell updates/sec

Title: US-09-941-947a-2

Perfect score: 2284

Sequence: 1 DYVTPYHITADIRFCHWTF.....FNSMLSEIQPKGKNEVSH 437

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1314	57.5	403 1	PPF_PROPR
2	311	13.6	342 1	K6P1_STRCO
3	305	13.4	346 1	PPF_DICTH
4	298.5	13.1	341 1	PPF_AMYMB
5	281.5	12.3	341 1	K6P1_STRCO
6	274.5	12.0	341 1	PPF_AMYMD
7	271.5	11.9	341 1	K6P1_STRCO
8	253	11.1	319 1	K6P1_THEMA
9	246.5	10.8	387 1	K6P1_YEAST
10	245.5	10.7	992 1	K6P1_KUOLA
11	242	10.6	319 1	K6P1_CLOPE
12	240.5	10.5	320 1	K6P1_SALTY
13	238.5	10.4	320 1	K6P1_ECOLI
14	234.5	10.3	327 1	K6P1_YERPE
15	233.5	10.2	322 1	K6P1_BACMC
16	233	10.2	319 1	K6P1_LACDE
17	230	10.1	322 1	K6P1_FUSNN
18	229.5	10.0	320 1	K6P1_ENTCL
19	226	9.9	322 1	K6P1_THBTL
20	224.5	9.8	329 1	K6P1_DHIRA
21	223.5	9.8	319 1	K6P1_BACHD
22	223.5	9.8	320 1	K6P1_BUCBP
23	223.5	9.8	320 1	K6P1_VIBCH
24	223	9.8	343 1	K6P1_MYCTO
25	222	9.7	340 1	K6P1_LACLA
26	222	9.7	320 1	K6P1_YARLI
27	220.5	9.7	320 1	K6P1_BUCAP
28	220	9.6	779 1	K6P1_RABIT
29	216.5	9.5	319 1	K6P1_CIOAB
30	216	9.5	337 1	K6P1_STRP8
31	216	9.5	337 1	K6P1_STRP8
32	216	9.5	337 1	K6P1_STRPY
33	216	9.5	784 1	K6P1_MOUSE

34	215	9.4	335 1	K6P1_STRPN	Q97rc6 streptococc
35	214.5	9.4	339 1	K6P1_STRPR	Q919e3 streptococc
36	213.5	9.3	321 1	K6P1_AQUAE	O67605 aquiflex ae
37	213.5	9.3	775 1	K6P2_ASFOR	Q9b920 aspergillus
38	212	9.3	781 1	K6P1_CANPA	P52784 canis famli
39	211	9.2	779 1	K6P1_MOUSE	P47857 mus musculu
40	210.5	9.2	320 1	K6P1_BUCAI	P57391 buchnera ap
41	210.5	9.2	343 1	K6P1_MYCIS	O33106 mycobacteri
42	210	9.2	779 1	K6P1_HUMAN	P08237 homo sapien
43	210	9.2	789 1	K6P1_HABCO	Q27665 haemophilu
44	210	9.2	987 1	K6P1_CANAL	O94201 candida alb
45	209	9.2	319 1	K6P1_BACST	P00512 bacillus st

ALIGNMENTS

RESULT 1
PPF_PROPR STANDARD; PRT: 403 AA.

AC P29495;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Phosphatase--fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90)
DE (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-
DE dependent 6-phosphofructose-1-kinase) (Pfi-dependent
DE phosphofructokinase) (Pfi-PFK).
GN PPF OR PFK.
OS Propionibacterium freudenreichii shermanii.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
OX NCBI_Taxid=1752;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91358443; PubMed=1653240;
RA Lador U.S., Gollapudi U., Tripathi R.L., Latschaw S.P., Kemp R.G.;
RT "Cloning, sequencing, and expression of pyrophosphate-dependent
RT phosphofructokinase from Propionibacterium freudenreichii."
RL J. Biol. Chem. 266:16550-16555(1991).
RN [2]
RP IDENTIFICATION OF CRITICAL LYSYL RESIDUES.
RX MEDLINE=92273593; PubMed=1117210;
RA Green P.C., Latschaw S.P., Lador U.S., Kemp R.G.;
RT "Identification of critical lysyl residues in the pyrophosphate-
RT dependent phosphofructo-1-kinase of Propionibacterium
RT freudenreichii."
RL Biochemistry 31:4815-4821(1992).
RN [3]
RP BIOCHEMICAL ACTIVITY: Diphosphate + D-fructose 6-phosphate =
RN phosphate + D-fructose 1,6-bisphosphate.
RN [4]
RP ENZYME REGULATION: NON-ALLOSTERIC.
RN [5]
RP PATHWAY: Key control step of glycolysis.
RN [6]
RP SUBUNIT: Homodimer.
RN [7]
RP SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY. PPF
SUBFAMILY.

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DR EMBL: M67447; AAA25675.1; -
DR PIR: A41169; A41169.
DR InterPro: IP0000023; Ppfckinase.
DR Pfam: PF00365; PFK.1.
DR PRINTS: PR00476; PPFCKTKINASE.
DR ProDom: PD000707; Ppfckinase; 1.
DR Transferrase; Kinase.
FT INIT MET 0
FT NP_BIND 120 125 PYROPHOSPHATE (POTENTIAL).

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PT ACT_SITE 150 150 NUCLEOPHILE (POTENTIAL);
SQ SEQUENCE 403 AA; 43114 MW; 1DE3272BA42B6E CRC64;
Query Match 57.5%; Score 1314; DB 1; Length 403;
Best Local Similarity 62.6%; Pred. No. 1,2e-81;
Matches 248; Conservative 60; Mismatches 88; Indels 0; Gaps 0;

QY 33 KKVAILTAGLAPCLNSAIGSLERITIEDPSIIBICRGYKGLLGDSPVTAVERKK 92
DB 2 KKVAILTAGLAPCLNSAIGSLERITIEDPSIIBICRGYKGLLGDSPVTAVERKK 61
QY 93 AGVLFQRFSSVINGSRKLTNVNDCVKGGLWKEGEPQKAAAOGLYKDGVDLHTIGSD 152
DB 62 YDPLRFSSGSPINGSRKLTNVNDCVKGGLWKEGEPQKAAAOGLYKDGVDLHTIGSD 121
QY 153 TMTAADLAAFLARNNGYLTGIPKTVNDVFPKISGLGAWTAQAGARYFNVAERN 212
DB 122 TMTAADLAAFLARNNGYLTGIPKTVNDVFPKISGLGAWTAQAGARYFNVAERN 181
QY 213 ANERMLIVHEWGRNGMTLAAFAOERYKLLDPAEWLPGLTRESYEVHAAVPEMAID 272
DB 182 AAFRELIHEWGRNGMTLAAFAOERYKLLDPAEWLPGLTRESYEVHAAVPEMAID 241
QY 273 LESAARGLREWMDKVCNIFVSEGAWEBAIVAEQAKGEVPRDAFGHILKLDANVRKM 332
DB 242 LDEAFRLRRTVMDEGVSNIPISEGAGVPDIAVQMGATGVEVTDAGHVDKXINPGAM 301
QY 333 FGSQFQMTGAKETLYVQSGYFPAASAVNDKRLIKSCADLAWECAFRRESGVIGHED 392
DB 302 FASQFQMTGAKETLYVQSGYFPAASAVNDKRLIKSCADLAWECAFRRESGVIGHED 361
QY 393 NGWVLAIFEPRIKGGKPFNIDTDMNSMLSEIGOP 428
DB 362 AGDKLSVIDPKRIAGHKPFIDTDMNSMLSEIGOP 397

RESULT 2
K6PL_STRCO STANDARD; PRT; 342 AA.
AC 008333;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphofructokinase 1 (EC 2.7.1.11) (Phosphofructokinase 1)
GN (Phosphohexokinase 1) (ATP-PFK).
DS PFK1 OR PFK1 OR PFK1 OR SC02119 OR SC02119.13C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Streptomycetales; Streptomycetaceae; Streptomyces.
ON NCBI_TaxID=1902;
RX MEDLINE=97208211; Pubmed=9055413;
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=A3(2) / 1109;
RA Holmes A.M.C.R., Ewerink G.J.W., Bibb M.J., Dijkhuizen L.;
RT Identification of ATP-dependent phosphofructokinase as a regulatory
RT step in the glycolytic pathway of the actinomycete Streptomyces
RT coelicolor A3(2).
RL Appl. Environ. Microbiol. 63:956-961 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=2196440; Pubmed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares K., Squares S., Taylor K.,
RA Warren T., Wierzejewski A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces

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RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY
CC PHOSPHOENOLPYRUVATE.
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SUBUNIT: Homotrimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
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CC -----
DR EMBL: U51728; AAC45135.1; -.
DR EMBL: AL938111; CAB51967.1; -.
DR PIR: T35500; T35500.
DR HSSE: P00512; 3PFR.
DR HAMAP: MF_00339; -.
DR InterPro: IPR000023; Pfrfructokinase.
DR Pfam: PF00365; PFRK.
DR PRINTS: PR00476; PFRCTKINSE.
DR ProDom: PD000707; Pfrfructinase.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
DR Kinase: Transferrase; Glycolysis; Multigene family; Allosteric enzyme;
DR Complete proteome.
SQ SEQUENCE 342 AA; 36664 MW; CEEFC7B74092AB34 CRC64;

Query Match 13.6%; Score 311; DB 1; Length 342;
Best Local Similarity 27.4%; Pred. No. 5,1e-14;
Matches 105; Conservative 63; Mismatches 137; Indels 78; Gaps 17;

QY 34 KKVAILTAGLAPCLNSAIGSLERITIEDPSIIBICRGYKGLLGDSPVTAVERKK 93
DB 2 KKVAILTAGLAPCLNSAIGSLERITIEDPSIIBICRGYKGLLGDSPVTAVERKK 61
QY 94 GYLQRFSSVINGSRKLTNVNDCVKGGLWKEGEPQKAAAOGLYKDGVDLHTIGSD 153
DB 59 GYLQRFSSVINGSRKLTNVNDCVKGGLWKEGEPQKAAAOGLYKDGVDLHTIGSD 105
QY 154 TMTAADLAAFLARNNGYLTGIPKTVNDVFPKISGLGAWTAQAGARYFNVAERN 213
DB 122 TMTAADLAAFLARNNGYLTGIPKTVNDVFPKISGLGAWTAQAGARYFNVAERN 181
QY 213 ANERMLIVHEWGRNGMTLAAFAOERYKLLDPAEWLPGLTRESYEVHAAVPEMAID 273
DB 182 AAFRELIHEWGRNGMTLAAFAOERYKLLDPAEWLPGLTRESYEVHAAVPEMAID 241
QY 273 LESAARGLREWMDKVCNIFVSEGAWEBAIVAEQAKGEVPRDAFGHILKLDANVRKM 332
DB 242 LDEAFRLRRTVMDEGVSNIPISEGAGVPDIAVQMGATGVEVTDAGHVDKXINPGAM 301
QY 333 FGSQFQMTGAKETLYVQSGYFPAASAVNDKRLIKSCADLAWECAFRRESGVIGHED 392
DB 302 FASQFQMTGAKETLYVQSGYFPAASAVNDKRLIKSCADLAWECAFRRESGVIGHED 361
QY 393 NGWVLAIFEPRIKGGKPFNIDTDMNSMLSEIGOP 428
DB 362 AGDKLSVIDPKRIAGHKPFIDTDMNSMLSEIGOP 397

RESULT 3
K6PL_STRCO STANDARD; PRT; 346 AA.
AC 09K471;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

```

D3 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90)
D3 (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-
D3 dependent 6-phosphofructose-1-kinase) (Ppi-dependent
D3 phosphofructokinase) (Ppi-PFK).
OS Dictyoglomus thermophilum.
OC Bacteria; Dictyoglom; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
OX NCBI_TaxID=14;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=RC46 B.1;
RX MEDLINE=20372656; PubMed=10913106;
RA Ding Y.-H.R., Rommus R.S., Morgan H.W.,
RT "Sequencing, cloning, and high-level expression of the pfp gene,
RT encoding a ppi-dependent phosphofructokinase from the extremely
RT thermophilic eubacterium Dictyoglomus thermophilum.";
RL J. Bacteriol. 182:4661-4666(2000).
CC -i CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
CC phosphate + D-fructose 1,6-bisphosphate.
CC -i PATHWAY: Key control step of glycolysis.
CC -i SIMILARITY: Belongs to the phosphofructokinase family.
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CC
CC EMBL; AF568276; AAF60100.1;
CC HSSP; P06998; 2PKF.
CC HAMAP; MF_00339; -; 1.
CC InterPro; IPR000023; Pfruckinase.
CC Pfam; PF00365; PFK; 1.
CC PRINTS; PR00476; PFRCTKINASE.
CC PRODOM; PD000707; Pfruckinase; 1.
CC PROSITE; PS00433; PHOSPHOFRUCTOKINASE; FALSE_NEG.
CC KINASE; Transferase; Glycolysis.
CC KW
CC SEQUENCE 346 AA; 37448 MW; 50C03B64BA7927F1 CRC64;

Query Match 13.4%; Score 305; DB 1; Length 346;
Best Local Similarity 27.5%; Pred. No. 1,3e-13;
Matches 107; Conservative 73; Mismatches 155; Indels 54; Gaps 15;

QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLGDSPYTAERKKA 93
DB 5 RIGVLTGGGDCPGLNPAIRGIWMR-ALDYDEVITGLKYGWAGLLKADTWPLSIEWED- 61

QY 94 GVLORFGSVIGNSRVKLTNVKDCVKGGLVKEGDPQKVNADQLVKGVDILHTIGDDT 153
DB 62 --LIEIGTLIGSSR---TNP-----FKCEDVYK-CYENKKNLMDALLAIGEDT 107

QY 154 NTAADLAFLAARNNGELFTVIGLPTVDNDVFPFKOSLGANTAAEGARYPNNVAENNA 213
DB 108 LGVASKR-----SKGLGPMIGVPTKIDKLEEDTDTGFTAVEVVDAIKRLDPTARS 161

QY 214 NPMRLIVHEVNGRNGMTLATAOYERKLLDBAEMLPELGLTRSEYVAHVPEMAIDL 273
DB 162 HARIIV-ELMGKRAAGMAL-----YGLAGAGDY-----ILIPVEAPNL 200

QY 274 EAEAKRLREVMKRVDCVNI FVSEAGVEALVAEMOKGQEVPRDAFGHIKLDVNGKMP 332
DB 201 EDLTNRHARKIYARARNNAVAIAEGVOLPGFTYQ--KQEGMVDADFGHIRLGGV--GNV 255

QY 333 FGEOPAMIGAEKTLVQSGVPARASASNDPMRLISCDLAECAFRBSGVTIGDED 392
DB 256 LAEITQNLGILETRAVALIS-HLQGGSPSIRDRIMGLLGRKADVLVBKSGILF--VAV 312

QY 393 KGNVLAIEEPRIKGPFPNIDTWMFNSM 421
DB 313 KGNELVAVPDITLIE-GTKKVDPAFESSV 340

RESULT 4
PFP_AMYME
ID PFP_AMYME STANDARD; PRT; 341 AA.
AC Q59126;
DT 15-JUN-1998 (Rel. 36, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90)
DE (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-
DE dependent 6-phosphofructose-1-kinase) (Ppi-dependent
DE phosphofructokinase) (Ppi-PFK).
DE PFP.
GN
OS Amycolatopsis methanolic.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=1814;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96125240; PubMed=8550409;
RA Alves A.M., Meijer W.G., Vrijbloed J.W., Dijkhuizen L.;
RT "Characterization and phylogeny of the pfp gene of Amycolatopsis
RT methanolic encoding ppi-dependent phosphofructokinase.";
RL J. Bacteriol. 178:149-155(1996).
CC -i CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
CC phosphate + D-fructose 1,6-bisphosphate.
CC -i PATHWAY: Key control step of glycolysis.
CC -i SUBUNIT: Homotetramer.
CC -i SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
CC EMBL; U31277; AAB01683.1; ALT_INIT.
CC HSSP; P00512; 3PKF.
CC HAMAP; MF_00339; -; 1.
CC InterPro; IPR000023; Pfruckinase.
CC Pfam; PF00365; PFK; 1.
CC PRINTS; PR00476; PFRCTKINASE.
CC PRODOM; PD000707; Pfruckinase; 1.
CC PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
CC KINASE; Transferase; Glycolysis.
CC KW
CC SEQUENCE 341 AA; 36229 MW; 306613246172D36B CRC64;

Query Match 13.1%; Score 298.5; DB 1; Length 341;
Best Local Similarity 28.8%; Pred. No. 3.5e-13;
Matches 108; Conservative 59; Mismatches 147; Indels 61; Gaps 16;

QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRGYKGLLGDSPYTAERKKA 93
DB 2 RIGVLTGGGDCPGLNPAIRGIWMR-ALDYDEVITGLKYGWAGLLKADTWPLSIEWED- 59

QY 94 GVLORFGSVIGNSRVKLTNVKDCVKGGLVKEGDPQKVNADQLVKGVDILHTIGDDT 153
DB 60 -ILIR-GGTLIGSSR---TNP-----YKBSGVEKTRA-VLADQGYDALAIGEDT 105

QY 154 NTAADLAFLAARNNGELFTVIGLPTVDNDVFPFKOSLGANTAAEGARYPNNVAENNA 213
DB 106 LGVAKKL-----TDGIGVGVPTKIDMDLAATDTGFTDRAVHATEAIBRLRTARS 159

QY 214 NPMRLIVHEVNGRNGMTLATAOYERKLLDBAEMLPELGLTRSEYVAHVPEMAIDL 273
DB 160 HIRAVV-ELMGKRAAGMAL-----YGLAGAGDY-----ILIPVEAPNL 198

QY 274 EAEAKRLREVMKRVDCVNI FVSEAGVEALVAEMOKGQEVPRDAFGHIKLDVNGKMP 333
DB 199 EGVNEMVERFERKMTAPIIVAGGAVPBG-GAVLARTGS---KDAFGHQLGGV--GTWL 252

```

QY 334 GEGPOMIGAKETLVKSGYFAPASASNDMDRLIKSCADLAVECAFRESGVIGHEBN 333
DB 253 ADEIAERTGESRAV-VLGHVQRGSTPAVDRLVATFGLHAYDAV-----ADGDF 302
QY 394 GNV--LRAIEFRRIK 406
DB 303 GTWALRGSTDLVRVK 317

RESULT 5
K6P3_STRCO
ID K6P3_STRCO STANDARD; PRT; 341 AA.
AC Q9RC39;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphofructokinase 3 (EC 2.7.1.11) (Phosphofructokinase 3)
GN PFK3 OR PFK3 OR SC01214 OR 2SCG58.14.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.D., James K.D., Harris D.B., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietorzek A., Woodward J., Barrill B.G., Parkhill J.,
RA Hopwood D.A.;
RA "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
CC -|- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -|- PATHWAY: Key control step of glycolysis.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
CC EMBL: AL939108; CAC01496.1; -
CC HSSP: P00512; 3PFK.
CC HAMAP: MF_00339; -; 1.
CC InterPro: IPR000023; Pfruckinase.
CC Pfam: PF00365; PFK; 1.
CC PRINTS: PR00476; PFRCTKINASE.
CC ProDom: PD000707; Pfruckinase.
CC DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
CC KINASE, Transferase; Glycolysis; Multigene family; Complete proteome.
CC KW SEQUENCE 341 AA; 36431 MW; E3050D37BD6F9F0 CRC64;
SQ

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QY 34 KAVILLAGLAPLNAIGSLIRYELIPISITICRGYKGLLGDSPYPTAERKKA 93
DB 2 RIVGLVSGGCPPLNAVIRSVAR-AVVDHGDVIGFRGWMKGLLECDY--LKLDDAVG 58
QY 94 GVLQRRGSGVIGSRVYLTVKDCVARGVKEGDEPQVAADQLVMDVILHTIGDDT 153

Query Match 12.3%; Score 281.5; DB 1; Length 341;
Best Local Similarity 26.8%; Pred. No. 5e-12;
Matches 100; Conservative 66; Mismatches 152; Indels 55; Gaps 12;

154 NTPAADLAALFARNVYGLVIGLPTKVDVDFPIQISGAMTAAEGGARYFMVVAENNA 213
DB 106 LKAAKRL-----SDNGLPVGVPTINDVAVTDTYTFPTAVVATALRLKTTAS 159
QY 214 NPPMLIVHEVMGRNCGMLTAAVQAEYRKLDRAEWLPELGLTRESYVAVFPENALDL 273
DB 160 HQRLVIV-EVMGRHTGMIALHSGM-----AAGAAVAVVPERPFDI 198
QY 274 EAEAKRLPYMKVDCUNVIFV-SBAGVPAIYAEQAGQVPRPAFGHILKIDAVRGM 332
DB 199 DELTAKVGRFSAAGRFPAIIVAAGAKKAGTMDDEG---KUYGHERPAGI--ARQ 252
QY 333 PEGPOMIGAKETLVKSGYFAPASASNDMDRLIKSCADLAVECAFRESGVIG 388
DB 253 LSELIEERLGRKARRV-ILGHVQRGSTPAVDRLVATFGLHAYDAVVAVHGEFGKPTALRG 311
QY 389 HDEDNGNVIRLRIE 401
DB 312 TDIENVSLADAVE 324

RESULT 6
PFP_AMPND
ID PFP_AMPND STANDARD; PRT; 341 AA.
AC Q9AGC0;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90)
DE 6-phosphofructokinase, pyrophosphate dependent (Pyrophosphate-
DE dependent 6-phosphofructose-1-kinase) (Ppi-dependent
DE phosphofructokinase) (Ppi-PFK).
GN PFP.
OS Amycolatopsis mediterranei (Nocardia mediterranei).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=33910;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S699;
RA Kuan L., Mueller M., August P.R., Pogosova-Agadjanyan E., Floss H.G.,
RA Yu T.;
RA "Characterization and cloning of three 3-deoxy-D-arabinopulsonate
RT 7-phosphate synthase isoenzymes from Amycolatopsis mediterranei
RT S699.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
CC phosphate + D-fructose 1,6-bisphosphate.
CC -|- PATHWAY: Key control step of glycolysis.
CC -|- SUBUNIT: Homotrimer (By similarity).
CC -|- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
CC EMBL: AF36847; AAK28147.1; -
CC HSSP: P00512; 3PFK.
CC HAMAP: MF_00339; -; 1.
CC InterPro: IPR000023; Pfruckinase.
CC Pfam: PF00365; PFK; 1.
CC PRINTS: PR00476; PFRCTKINASE.
CC ProDom: PD000707; Pfruckinase.
CC DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
CC KINASE, Transferase; Glycolysis.
CC KW SEQUENCE 341 AA; 36272 MW; 2B5C28E7BBD57065 CRC64;
SQ

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EMBL, AL939123; CAB72402.1; -

DR HSSP; P00512; 3EPK.

DR HAMAP; MF_00339; -; 1.

DR InterPro; IPR000023; Pfkinckinase.

DR Pfam; PF03365; PFK, 1.

DR PRINTS; PR00476; PFKCTKINASE.

DR PRODOM; PD000707; Pfkkinckinase; 1.

DR PROSITE; PS00433; PHOSPHOFUCTOKINASE; 1.

DR KINASE; Transferase, Glycolysis; Multigene family; Complete proteome.

SEQUENCE 341 AA; 36433 MW; 6C0809B76FE90BBD CRC64;

Query Match 11.9%; Score 271.5; DB 1; Length 341;
Best Local Similarity 26.4%; Pred. No. 2.4e-11;
Matches 97; Conservative 59; Mismatches 132; Indels 79; Gaps 15;

QY 34 KALLITGGALAPCLNSAIGSLIERYTEIDSIETICRYGGYKLLGDYSVTAEVRKA 93
DB 2 RIGVLITGSGDCPGNNAIRSVARAAD-NGDEVTIGFEDTAGILL--DGRRALDIANA 58
QY 94 GVLGRFGSGVYIGNSRYELTNVKDCYKRGVYKGEHPQKVAADQYKDGVDILHTIGDDT 153
DB 59 GILAR--GGTIGSSRLTRDLRLREACEN-----AGDMIGNFGIDALIPIGEGT 105
QY 154 NTLAADLAFLARNRYLTLYTGPKTYDNDVDFPKQSLGAWTAADQGARFMVAENNA 213
DB 106 LTAARML-----SDAGLPVAGVPEKTIIDNDISSTDRFFGPDYAGVATEANDRUKTTA 159
QY 214 NPRRLIVHEWVGNCGMLTATATQEVKLLDRAEWLPETLTRESYEVHAFVEMAI 273
DB 160 HGRNMY-ELWGHAGIAL-----ESGMAGCA---HGICLPERFPD 198
QY 274 EAERKRLREVMDC---VDCNIVFVSEGA-----GVEAIVAEWQAKGQEVPRDAF 319
DB 199 ADLVKWEVERFSSGKKFAYVC---VAEGHAPAGSMDYKGA1-----DKF 241
QY 320 GHITLDVNVGKMFGEQFAQMIGAE-KTLQKSGYFARASASVNDWRLIKSCADLAVEC 378
DB 242 GHERFGSIGTALAP--ELERLKEAKPEVI--LGEVORGGVPRAYADVLAITRGMAVEA 297
QY 379 AFRRESG 385
DB 298 AHRGDFG 304

RESULT 8
KEPF THEME
ID KEPF THEME STANDARD; PRT; 319 AA.
AC O9WY52;
DE 16-OCT-2001 (Rel. 40, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-Phosphofructokinase (BC 2.7.1.11) (Phosphofructokinase)
DE (Phosphoenolpyruvate carboxylase)
DE PFKA OR TM0209.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN 11

SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RC MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Cotton M.D., Pratt M.J., Linder C.A., Garrett M.M.,
RA Stewart A.M., Utterback T.R., Malek J.A., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.C., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
evidence for lateral gene transfer between Archaea and Bacteria from

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RT genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
DR EMBL: AE001705; AAD5301.1; -.
DR PIR: C72406; C72406.
DR HSSP: P00512; 3PFK.
DR TIGR: TMO208; -.
DR HAMMP: MF_00339; -.
DR InterPro: IPR000023; Pfruckinase.
DR Pfam: PF00365; PFK.
DR PRINTS: PR00476; PFRCKTNASE.
DR PRODOM: PD000707; Pfruckinase.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
DR KINASE: Transferase; Glycolysis; Complete proteome.
SQ SEQUENCE 319 AA; 34487 MW; 3809B97128BD1288 CRC64;

Query Match 11.1%; Score 253; DB 1; Length 319;
Best Local Similarity 26.6%; Pred. No. 3.9e-10;
Matches 95; Conservative 60; Mismatches 126; Indels 76; Gaps 14;

QY 33 KRAVITAGGLAPCLNSAIGSLIERTEIDPSIEITICRGYKGLLGDSYPTAVREK 92
DB 2 KKAIVITSGDAGMNAVAAY-RY-GVAGQLEIVGVRGSGGLDGF-VKLEKOV 57
QY 93 AGVLOFGSGVINSRVKLTNVDCVKGKLVKKEGPOKVAADQVKGDDIHTIGEDD 152
DB 58 AGITER-GGITATISCEBEKT-----EGRELAQAQIKGHGIVIGSG 104
QY 153 TTTAAADLAAFLARNYGLTVGLPTVDNDFPIQSLGAMTAAGGARYFNVAERN 212
DB 105 SLT-----GAILLYEESHKIPVVGIPATIDMDIGLTMCGVDTCENTVMDAVOKLDTAS 159
QY 213 ANRPMIVHEVMGRCNGWLTAAVAOERYKLDRAEMLPELGLRESYEVHVAVPEMATD 272
DB 160 SHERATIV-EVMGRHSGYILMAG-----LVTCAB-----AIVPEIPVD 198
QY 273 LEAEANRLAEV-MDRVDCVNIFVSEAGAVEALVAEMQAQGEVPRDAGHTKLDVNG 330
DB 199 YSOLADRIELEERRGRKINSI-ILVAGGAASAYTVAR-----HLE----- 236
QY 331 KMGEGEACMGIAEKTEIVQSGGFARASASANDMLIISCADLAIEGAFRRPSGYI 387
DB 237 -----YRIGYE-EKITILGHVQSGSPTAFDRRLASMGVEAVDALDGEVDW 284

RESULT 9
K6P1_YEAST
ID K6P1_YEAST STANDARD; PRT; 987 AA.
AC P16861;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB 6-phosphofructokinase alpha subunit (EC 2.7.1.11) (Phosphofructokinase
DE 1) (Phosphohexokinase) (6pfr-1-K alpha subunit).
GN PFK1 OR YGR240C OR G859.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=89378757; PubMed=2528496;
RA Heintsch J.J., Ritzel R.G., von Borsel R.C., Aguilera A.,
RA Rodicio R., Zimmermann F.K.;
RT "The phosphofructokinase genes of yeast evolved from two duplication
RT events";
RL Gene 78:309-321(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97245298; PubMed=9090057;
RA Guerreiro P., Azevedo D., Barreiros T., Rodrigues-Pousada C.;
RT "Sequencing of a 9.9 kb segment on the right arm of yeast chromosome
RT VII reveals four open reading frames, including PFK1, the gene coding
RT for sucinyl-CoA synthetase (beta-chain) and two ORFs sharing
RT homology with ORFs of the yeast chromosome VII.";
RL Yeast 13:275-280(1997).
RN [3]
RP SEQUENCE OF 794-987 FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=96267763; PubMed=8701610;
RA van der Aart Q.U.M., Kleine K., Steensma H.Y.;
RT "Sequence analysis of the 43 kb CRM1-YLM9-BET54-DIE2-SM1-PHO81-YHB4-
RT PFK1 region from the right arm of Saccharomyces cerevisiae chromosome
RT VII.";
RL Yeast 12:385-390(1996).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- ENZYME REGULATION: Allosterically inhibited by ATP and activated
CC by AMP and fructose 2,6-bisphosphate (By similarity).
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SUBUNIT: Heterodimer of 4 alpha and 4 beta chains.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the phosphofructokinase family. Two domains
CC subfamily.
CC
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CC
DR EMBL: M26943; AAA34859.1; -.
DR EMBL: Z73025; CA97268.1; -.
DR EMBL: X87941; CA61193.1; -.
DR PIR: J00016; J00016.
DR HSSP: P00512; 3PFK.
DR SGD: S0003472; PFK1.
DR GO: GO:0005945; C:6-phosphofructokinase complex; IMP.
DR GO: GO:0005737; C:cytoplasm; IDA.
DR GO: GO:0003872; F:6-phosphofructokinase activity; IMP.
DR InterPro: IPR000023; Pfruckinase.
DR Pfam: PF00365; PFK.
DR PRINTS: PR00476; PFRCKTNASE.
DR PRODOM: PD000707; Pfruckinase.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 2.
DR KINASE: Transferase; Glycolysis; Repeat; Allosteric enzyme.
SQ SEQUENCE 987 AA; 107970 MW; 995B3DFC7781B29 CRC64;

Query Match 10.8%; Score 246.5; DB 1; Length 987;
Best Local Similarity 23.9%; Pred. No. 4.3e-09;
Matches 103; Conservative 68; Mismatches 135; Indels 125; Gaps 19;

QY 31 KPKVAVITAGGLAPCLNSAIGSLIERTEIDPSIEITICRGYKGLLGDSYPTAVR 90
DB 204 KKKKIAVMTSGDSDGMNAVAAYR-TG-IHFGCDVAVVAGYGLLRGKGY-----LK 256
QY 91 KKA-----GVLOFGSGVINSRVKLTNVDCVKGKLVKKEGPOKVAADQVKGDDI 145
DB 257 KKAIVITSGDAGMNAVAAYR-----RSMERFRKRGKRAAGNLISGIDAL 303

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QY 146 HTIGEDDTNTAAADL-----AALFARNY-----GLTVIGLPTVDNDVPFI 187
 DB 304 VVCGGDGSLT-GNDLFRHEWPSIVDELVAEGRTTEEVAPYKNTIVGLVSDIDMDSGT 362
 QY 188 KOSLGAMTAEGGARYFMNVAVENNANPMLIVHEWGRNCGMLT-----AATQOEYKLL 243
 DB 363 DSTIGAYSALEERICEMVDYIDATAKSHSRAFYV-EVWGRHCGMLLMGLIATGADY---- 417
 QY 244 DDAEMLPGLTRRESYEVAVFPEKAILDEAKRLREMDKVCV-----NIVYSGA 298
 DB 418 -----IFIPRAVPHGKQDELEKEVCQRHSKGRNNITIIAEGCA 457
 QY 299 -----GVEAIVAEWQAKQGEVPRDAFHIKL--DAVNPGRKFGQEPQMGIGAEK 345
 DB 458 LDDQAMPYANVYKALIEL-----GLDTKTITIGHVGRGTAVAHDRMLAT--LQGVDAVK 512
 QY 346 TVQKSGYARASASN-----VDMKRLIKSCADLAVECAFRESGVIGDE 391
 DB 513 AVLE-----FTPEPSPILIGLENKILRMVLVESVLTSAV-----TALENDF 557
 QY 392 DNGNVLRAIEF 402
 DB 558 DKATSLRDTDF 568

RESULT 10
 K6PF_KLULA STANDARD; PRT; 992 AA.

AC 003215;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 6-phosphofructokinase alpha subunit (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (6PF-1-K alpha subunit).
 GN PFKL.
 OS Kluveromyces lactic (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=9331653; Pubmed=8326866;
 RA Heinisch J.J., Kirchbach L., Liesen T., Vogelens K., Hollenberg C.P.;
 RT Molecular genetics of phosphofructokinase in the yeast Kluveromyces lacticus.";
 RL Mol. Microbiol. 8:559-570(1993).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
 CC -1- ENZYME REGULATION: Allosterically inhibited by ATP and activated by AMP and fructose 2,6-bisphosphate.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBUNIT: Heterodimer of 4 alpha and 4 beta chains.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family. Two domains subfamily.
 CC -----
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 CC -----
 CC EMBL: Z17315; CA78963.1; .
 CC DR PIR: S32902; S32902.
 CC DR HSSP: P00512; 3PFK.
 CC DR InterPro: IPR000023; Pfruckinase.
 CC DR Pfam: PF00365; PFK; 2
 CC DR PRINTS: PR00476; PFRCKINASE.
 CC DR PRODOM: PD000707; Pfruckinase; 2.
 CC DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 2.
 CC KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme.

SQ SEQUENCE 992 AA; 109336 MW; 724687850F277F9 CRC64;

Query Match 10.7%; Score 245.5; DB 1; Length 992;
 Best Local Similarity 23.8%; Pred. No. 5,16-09;
 Matches 108; Conservative 74; Mismatches 165; Indels 107; Gaps 19;

QY 30 NKPKVAILTPGALPCLNSALISGLIEREYDEISIEICRGQYKGLLDSPYATVAV 89
 DB 181 SKKKKLAWNTSGDSQGNAAVAVVR--SITYGCVAYAVYEGYVKGQDYLAKXEW 238
 QY 90 RKKAGVLRFGSGVYIGNSRVLTIVKDCVKGALKEGED--PKRYAADQVAKGVILHT 147
 DB 239 KDVAQWLSR--GGTLIGTAR-----SKERREWRGRQAQSNLIDQSIDLVY 283
 QY 148 IGEDDTNTAA-----ADLAFLARN-----YGLTVIGLPTVDNDVPFIKOS 190
 DB 284 IGGDGLTGLADLFSEWPSIVBELYKQKTEDEVALYQMLITVGMGWSIDNDMSGTST 343
 QY 191 IGAWTAEGGARYFMNVAVENNANPMLIVHEWGRNCGMLT-----TATQOEYKLLDRA 246
 DB 344 IGAYSALEERICEMVDYIDATAKSHSRAFYV-EVWGRHCGMLLMGLIATGADY----- 395
 QY 247 EMLPELGLTRSYEVAVFPEKAILDEAKRLREMDKVCVNTFVSEGA- 298
 DB 396 -----IFIPRAVPHGKQDELEKEVCQRHSKGRNN--TVIAGAL 436
 QY 299 --GVEAIVAEWQAK-----QGVPRDAFHIKL--DAVNPGRKFGQEPQMGIGAEKTV 348
 DB 437 DDQAMPYTAB-QVNDVIVELGLDPTKTTTIGHVGRGTAVAHDRMLAT--LQGVDAVRAIL 493
 QY 349 ----OKSGYARASASNVDMLIKSCADLAVECAFRESGVIGDEHNGNVLRAIEFPR 404
 DB 494 NMTPEPSPILIGLENKILRMVLVES-----VLTQVAAIAIKDKATSLRDTDFIE 548
 QY 405 I-----KGGKRPNDTFWNSMLSEIQGP 428
 DB 549 LYSNFMSTVNDGSQLPEADRLNTAIVAGAP 582

RESULT 11

K6PF_CLOPE STANDARD; PRT; 319 AA.

AC Q8XNH2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase) (phosphohexokinase).
 GN PFKA OR PFK OR CPO361.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / Type A.
 RX MEDLINE=21664373; Pubmed=11792842;
 RA Shimizu T., Ohnani K., Hirakawa H., Oshima K., Yamashita A., Siba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
 CC -----
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266 VPMAIDLEABK-----RLREVMKDVCNIFVSEGAVE--AIVAEMQAK 310

DB 201 -----DVAEIRAGIKKGGKHAIVATHEMCDVDELAHFIEKTEGRETATVAGHIORG 254
 QY 311 GQWEPDPAFGHIKLDVAVNPGWPGQAPOMIGAKTLVOKSGYFARASANDMDRLIKS 370
 DB 255 GSPVEYD-----RILASMGVAV-----272
 QY 371 CADLAV-----CAFRSEGVIGHDENGVNLAIEFPRIKGGKRPRIIDTW 417
 DB 273 -IDLILHGGRCRGVIGIONEDLVHDD-----ITDAIENMK---RPFK--SDW 312

RESULT 13
 K6P1_ECOLI
 ID K6P1_ECOLI STANDARD; PRT; 320 AA.
 AC P06936;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE 6-phosphofructokinase isozyme I (EC 2.7.1.11) (Phosphofructokinase-1)
 GN PFKA OR B3916 OR 25460 OR ECS4841 OR SF3994.
 OS Escherichia coli,
 OS Escherichia coli O157:H7, and
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 NCBI_TaxID=562, 83334, 623;
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=85203917; PubMed=3158524;
 RA Hellinga H.W., Evans P.R.;
 RT "Nucleotide sequence and high-level expression of the major
 RL Escherichia coli phosphofructokinase.";
 RL Eur. J. Biochem. 149:363-373(1985).
 RN
 RP REVISIONS, AND MUTAGENESIS.
 RC SPECIES=E.coli;
 RX MEDLINE=87229041; PubMed=2953977;
 RA Hellinga H.W., Evans P.R.;
 RT "Mutations in the active site of Escherichia coli
 RL phosphofructokinase.";
 RL Nature 327:437-439(1987).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=93347969; PubMed=8346018;
 RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
 RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
 RL region from 87.2 to 89.2 minutes.";
 RL Nucleic Acids Res. 21:3391-3398(1993).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boulton A., Siao Y., Miller L.,
 RA Grotbeck J.E., Davis N.W., Lim A., Dimalanta E.T., Potomousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7,"
 RL Nature 409:529-533(2001).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi W., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo H., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12,"

RL DNA Res. 8:11-22(2001).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Sun L., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao Y., Gao Y., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RL through comparison with genomes of Escherichia coli K12 and O157,"
 RL Nucleic Acids Res. 30:4432-4441(2002).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RC SPECIES=E.coli;
 RX MEDLINE=89125622; PubMed=2975709;
 RA Shitkaibara Y., Evans P.R.;
 RT "Crystal structure of the complex of phosphofructokinase from
 RL Escherichia coli with its reaction products.";
 RL J. Mol. Biol. 204:973-994(1988).
 CC
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
 CC fructose 1,6-bisphosphate.
 CC -1- ENZYME REGULATION: SUBJECT TO ALLOSTERIC ACTIVATION BY ADP AND
 CC OTHER DIPHOSPHONICLOSIDES, AND INHIBITION BY PHOSPHONOLPYRUVATE.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: E.COLI HAS TWO 6-PHOSPHOFRUCTOKINASES ENZYMES.
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
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 DR EMBL, X02519; CAA26356.1; -;
 DR EMBL, L19201; AAB03048.1; -;
 DR EMBL, AE000466; AAC76898.1; -;
 DR EMBL, AE005622; AAG59109.1; -;
 DR EMBL, AP002567; BAB38264.1; -;
 DR EMBL, AE015406; AAN45428.1; ALT_INIT.
 DR PIR, A86081; A86081.
 DR PIR, A98234; A98234.
 DR PIR, G65197; KIECPA.
 DR PDB, 1PFK; 15-OCT-92.
 DR PDB, 2PFK; 15-OCT-92.
 DR SWISS-2DPAGE; P06998; COLI.
 DR EC02DBASE; F035.8; 6TH EDITION.
 DR EcoGene; EG106599; PFKA.
 DR HAMAP; MF_003399; -; 1.
 DR InterPro; IPR000023; Pfrfructinase.
 DR Pfam; PF00365; PFK; 1.
 DR PRINTS; PR00476; PFRFRCTINASE.
 DR ProDom; PD000707; Pfrfructinase; 1.
 DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
 KW Kinase, Transferase, Glycolysis, 3D-structure, Allosteric enzyme,
 KW Complete proteome.
 FT ACT_SITE 128
 FT MUTAGEN 128 128
 FT MUTAGEN 172 172
 FT
 FT CONFLICT 74 74 P -> C (IN REF. 1).
 FT CONFLICT 103 104 GD -> DG (IN REF. 1).
 FT CONFLICT 163 163 R -> P (IN REF. 1).
 FT STRAND 317 319 KKL -> EKM (IN REF. 1).
 FT TURN 4 9
 FT TURN 15 16
 FT HELIX 17 30
 FT TURN 31 32

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FT STRAND 34 38
FT TURN 40 40
FT HELIX 41 46
FT TURN 47 48
FT STRAND 50 53
FT HELIX 56 58
FT TURN 59 60
FT TURN 62 63
FT TURN 68 69
FT HELIX 75 78
FT HELIX 80 92
FT TURN 93 94
FT STRAND 97 102
FT HELIX 104 115
FT TURN 116 117
FT STRAND 120 125
FT TURN 127 128
FT TURN 132 133
FT STRAND 138 138
FT TURN 139 139
FT HELIX 140 161
FT TURN 162 162
FT STRAND 164 169
FT TURN 172 173
FT HELIX 176 184
FT TURN 185 186
FT STRAND 189 191
FT TURN 193 194
FT HELIX 199 211
FT TURN 212 213
FT STRAND 217 222
FT HELIX 228 239
FT STRAND 243 247
FT HELIX 249 253
FT TURN 259 278
FT TURN 279 279
FT STRAND 283 288
FT TURN 289 290
FT STRAND 291 296
FT HELIX 297 303
FT HELIX 310 320
SQ SEQUENCE 320 AA; 34842 MW; D03D79F6A5536A41 CRC64;

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Query Match 10.4%; Score 238.5; DB 1; Length 320;
Best Local Similarity 24.9%; Pred. No. 3.7e-09;
Matches 100; Conservative 65; Mismatches 132; Indels 105; Gaps 18;

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QY 33 KKVAILTAGLAPCLNSAIGSLIERYTEIDPSIEITCTRGCKGL-----LIGDSYPTA 87
DB 3 KXIGVLTCGDAFGKNAAIRGVVR--SALTGELFVWGIVDEYGLIYEDRMVQLDRYSVSD 60
QY 88 EVRKKAAGVLRQFGGVSINSRVKLTNVDCVKGIVKEGDEPOKVAADQLVKDGVILHT 147
DB 61 MINR-----GGTFSSAR--PREFD-----ENIRAVAIENLKKRGIDALVY 100
QY 148 IGGDDTNTAAADLAFLARNNYGLTVIGLPKTVNDVFPKISGAMWTAEOGARYPNV 207
DB 101 IGGDSYVMAKRL-----TEMGFPCIGLPGIINDIKGTLYTIGFTALSTVVEALDRL 154
QY 208 VAENNANRMLIVHEWNGRCNMTLTAACNGBRKLLDAEW--LPELGLTESEYVNAHF 265
DB 155 RDTSSSHRISIV--EVMGRYCGDLTLAA-----IAGGCEVAVVEVPSFSD-----L 202
QY 266 VPEMAIDLEAEAKR-----LREVMDKVDCAVNIIVSEGAIVE--AIYAEQAKQEVPRD 317
DB 203 VNEIKAGI--AKGKKAIVAIITEHMDVDDELAFHEIKETGRTATVIGLHIGRGSSPYVD 261
QY 318 AFGRHKLDVAVDPGKPGGQZPACMTIAEKTIVQKSYFPAASAVNDMKILKSCADLAIVE 377
DB 262 RI-----LASRMGAIVAILDLAVYGR----- 283
QY 378 CAFRESGVIGHEDNGVTLAIEPPRIKGGKPFNIDMTWN 419

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DB 284 CAGIQNEQLVHED-----IIDAIENMK-----REFK--GDWLD 314

RESULT 14
K6PF YERP ID K6PF YERP STANDARD; PRT; 327 AA.
AC ORJ16;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE (Phosphohexokinase)
GN PKA OR YPO0078 OR Y0059.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_Taxid=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Penrice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.,
RA "Genome sequence of Yersinia pestis, the causative agent of plague,"
RT Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Lise P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.B., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
CC -1- CATALYTIC ACTIVITY: ADP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
CC
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CC
DR EMBL: AJ14141; CAC88944.1; -
DR EMBL: AE013607; AAM83654.1; -
DR PIR: AF0010; AF0010.
DR HAMAP: MF 00339; -. 1.
DR InterPro: IPR000023; PfRckKinase.
DR Pfam: PF00365; PFK. 1.
DR PRINTS: PR00476; PFRCKTKINASE.
DR ProDom: PD000707; PfrckKinase. 1.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
KW Kinase; Transferase; Glycolysis; Complete proteome.
SQ SEQUENCE 327 AA; 35394 MW; 1D54B3B8BD0E430D CRC64;

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Query Match 10.3%; Score 234.5; DB 1; Length 327;
Best Local Similarity 27.2%; Pred. No. 7.1e-09;
Matches 84; Conservative 50; Mismatches 102; Indels 73; Gaps 13;
QY 33 KKVAILTAGLAPCLNSAIGSLIERYTEIDPSIEITCTRGCKGLG-----DSYFPTA 87

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DB 3 KXIGVLTSGDADGNNAAIRGVVR--AALSAGLDVFGIEDYGLVYENRKKKIDRYSVD 60
 QY 88 EVKKKAGVORFGSGVYGNRKYLTNVKCCVYKGLVYEGSDPO--KYAADQLYKGDYDL 145
 DB 61 MNR-----GGTFLGSGAR-----PPEFRDPYVRKALNNMERIGDGL 98
 QY 146 HTTGDDDTTAAADIAFLARNYGLTVIGLPTVDNDVFPPIKOSIGAWTAAGARFYM 205
 DB 99 VVIGGDS-SYAGDILZ---KEGGHCVGLPGTINDVAGTDTTIGFTALLETVEAID 153
 QY 206 NVAVENNANRKLIVHEWGRNCGMLTAATAOYRKLDRAEW--LPELGLTESYEVAH 263
 DB 154 RLDTSSSSQRIISIV-EVMGRYCGDLTAA--IAGCEPIALPEVEFKSD----- 201
 QY 264 VFPEPAIDLEAEAK-----RLREVNDKDCVNIIVSEAGVY--AIYAEMQ 308
 DB 202 -----DLVAITKGIAGKKGKHAIVALTKEKDDIDSLAKYLEKERTGTGTGVLGHIO 253
 QY 309 AKGOEVPDR 317
 DB 254 RGAPVAYD 262

RESULT 15
 K6PF_BACMC STANDARD; PRT; 322 AA.

AC 059214;
 DT 15-JUL-1998 (Rel. 36, Last Created)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
 GN PFKA OR PFK.
 OS *Bacillus macquarientis*.
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
 OX NCBI_TaxID=1468;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23464;
 RX MEDLINE=96257193; Pubmed=8675031;
 RA Rouwendal G.J.A., Zwieters L.H., Wolbert E.J.H., Springer J.,
 RA Moolbroek H., Huizing H.J.;
 RA "Cloning, sequence and expression in *Escherichia coli* of the gene
 RT encoding phosphofructokinase from *Bacillus macquarientis*,"
 RL Gene 171:59-63(1996).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.
 CC -1- PATHWAY: Key control step of glycolysis.
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 CC EMBL: X76484; CAA54022.1; -.
 DR PIR: S19248; S39248.
 DR HSSP: P00512; 3PFK. 1.
 DR HAMAP: MF_00339; -; 1.
 DR InterPro: IPR000023; Pfkfrkinase.
 DR Pfam: PF00365; PFK, 1.
 DR PRINTS: PR00476; PHFRCTKINASE.
 DR ProDom: PD000707; Pfkfrkinase; 1.
 DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
 KW kinase, Transferase, Glycolysis.
 SQ SEQUENCE 322 AA; 34648 MW; 2C156F42669EC46C CRC64;

Query Match 10.2%; Score 233.5; DB 1; Length 322;

Best local similarity 25.2%; Pred. No. 8 le-09;
 Matches 101; Conservative 68; Mismatches 141; Indels 91; Gaps 17;
 QY 33 KXVAILTAGGLAPCLANSAGLIBRYTBIDPISIIICRGGYKGLLDGSPYTAVERKK 92
 DB 4 KXIAVLTSGDSDGNNAAVAVVR--SGLFYGLFVYGIQRYGILLNDIDF--SMDLRSV 59
 QY 93 AGVLRFGSGVYGNRKYLTNVKDCVYKGLVYEGSDPOKYAADQLYKGDYDLTIGSD 152
 DB 60 GDIQR-GGTVLQSR-----CKEFTPEG--QKQADILRKRGIDGLVYIGSDG 106
 QY 153 TMTAADIAPFARANNVGLTVIGLPTVDNDVFPPIKOSIGAWTAAGARFYMNVAAEN 212
 DB 107 SYHGNK-----SKGLNTMALPGTINDNDSTYDPTTIGFTSIVIVDALNKLRTMS 160
 QY 213 ANPRMLIVHEWGRNCGMLTAATAOYRKLDRAEWLPELGLTRSYEVAHVFPEPAID 272
 DB 161 SHERSSIV-EVMGRHCGDIAL---YAGLASGAS-----TIIVEVPPD 199
 QY 273 LEAAKRLRE--VMDKDCVNIIVSEAGVYEAIVAEQAKGOEVPDRAGHKLDVAVNG 330
 DB 200 MDEIARMKQNPFAHGRHSI-VVAEGAG-----NGENVAK----- 234
 QY 331 KMFGEQAFQMTGAEKTL---VQKSGYFARASAVNDMLIKSCADLAVECAFRES--- 384
 DB 235 -----QLVERCETLBPRTVVLGHIOGGTPTADRLARLDPAVRKMLIAGBSAVA 286
 QY 385 -GVIGHDEKGVYLAIEPPRIKGGKPPNIDDMNSHISE 424
 DB 287 CGII-----SNELVINDID-KVYNSKKEPMELYELAAHLSQ 322

Search completed: January 29, 2004, 14:37:01
 Job time : 18 secs

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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:30:22 ; Search time 40 Seconds
(without alignments)
2819.225 Million cell updates/sec

Title: US-09-941-947A-2

Perfect score: 2284
Sequence: 1 DVTMPYHLLADIRCHWPF.....FNSMLSEIGQKGVSH 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_rnc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_proteus:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1453	63.6	410	5 Q9NGP6	Q9NGP6 mastigamoeba
2	1302	57.0	404	16 Q92NK9	Q92NK9 rhizobium m
3	1292.5	56.6	514	16 Q8UDL0	Q8UDL0 agrobacteri
4	305	13.4	346	2 Q9KH71	Q9KH71 dictyoglomu
5	282	12.3	488	10 Q9FUT5	Q9FUT5 arabidopsis
6	281.5	12.3	485	10 Q9CS07	Q9CS07 arabidopsis
7	278	12.2	366	16 Q8XU57	Q8XU57 clostridium
8	274.5	12.0	341	2 Q9AGC0	Q9AGC0 amycolatops
9	270	11.8	448	16 Q94AA4	Q94AA4 borrelia bu
10	266	11.6	489	10 Q94AA4	Q94AA4 arabidopsis
11	263.5	11.5	436	5 Q97651	Q97651 entamoeba h
12	263.5	11.5	586	10 Q94J12	Q94J12 cryza sativ
13	260.5	11.4	775	10 Q94G72	Q94G72 cryza sativ
14	260	11.4	382	5 Q24812	Q24812 entamoeba h
15	257.5	11.3	500	10 Q9ST07	Q9ST07 arabidopsis
16	253	11.1	473	10 Q817L4	Q817L4 arabidopsis

17	252	11.0	459	2 Q8VU09	Q8VU09 amycolatops
18	252	11.0	487	5 Q15648	Q15648 trypanosoma
19	251	11.0	473	10 Q9M0F9	Q9M0F9 arabidopsis
20	250	10.9	426	5 Q61068	Q61068 trichomonas
21	248.5	10.9	437	5 Q27705	Q27705 naegleria f
22	245	10.7	324	2 Q8GNC1	Q8GNC1 haemophilus
23	245	10.7	431	16 Q8EXU6	Q8EXU6 leptospira
24	244.5	10.7	486	5 Q9BIC6	Q9BIC6 leishmania
25	243	10.6	462	10 Q9X076	Q9X076 arabidopsis
26	240.5	10.5	352	16 Q8FBD0	Q8FBD0 escherichia
27	240	10.5	337	1 Q57694	Q57694 thermoprote
28	239	10.5	452	10 Q8LA55	Q8LA55 arabidopsis
29	235	10.3	390	16 Q8KRS2	Q8KRS2 chlorobium
30	234	10.2	530	10 Q9FKG3	Q9FKG3 arabidopsis
31	232	10.2	461	16 Q83146	Q83146 treponema p
32	226.5	9.9	444	10 Q9F1K0	Q9F1K0 treponema p
33	223.5	9.8	921	5 Q8SSA3	Q8SSA3 encephalito
34	222.5	9.7	361	2 Q9S479	Q9S479 myxococcus
35	221	9.7	335	16 Q8DQ85	Q8DQ85 streptococc
36	221	9.7	490	5 Q8WPR2	Q8WPR2 trypanoplas
37	220	9.6	573	16 Q83553	Q83553 treponema p
38	218	9.5	750	4 Q96160	Q96160 homo sapien
39	217.5	9.5	320	16 Q8DCY1	Q8DCY1 vibrio vuln
40	217.5	9.5	537	10 Q8VYN6	Q8VYN6 arabidopsis
41	216	9.5	784	11 Q8C605	Q8C605 mus musculu
42	213.5	9.3	775	3 Q9H3Z0	Q9H3Z0 aspergillus
43	212.5	9.3	337	16 Q8DPR6	Q8DPR6 streptococc
44	212.5	9.3	549	2 Q9FAE8	Q9FAE8 porphyromon
45	212	9.3	784	11 Q8CS16	Q8CS16 mus musculu

ALIGNMENTS

RESULT 1	Q9NGP6	PREDIMINARY;	PRT;	410 AA.
ID	Q9NGP6			
AC	Q9NGP6			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DS	PPI-phosphotransferase (EC 2.7.1.11).			
GN	PPIPK.			
OS	Mastigamoeba balaamuthi (Phreatamoeba balaamuthi).			
OC	Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.			
OX	NCBI_TaxID=108607;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Lee J.A., Moore D., Sengen C.W., Gaasterland T., Muller M.,			
RT	"cDNA clones (expressed sequence tags) from the free-living			
RT	amitochondriate amoeboid flagellate Mastigamoeba balaamuthi."			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF246209; AAF70463.1; -			
DR	InterPro: IPR000023; PPIphosphotransferase.			
DR	Pfam: PF00365; PPK.1.			
DR	PRINTS; PR00476; PPIPKINASE.			
DR	ProDom; PD000707; PPIphosphotransferase; 1.			
KW	Kinase; Transferase.			
SO	SEQUENCE 410 AA; 44200 MW; CD362D1D2D41A0D0 CRC64;			
Query Match	63.6%; Score 1453; DB 5; Length 410;			
Best Local Similarity	67.2%; Pred. No. 2.8e-99;			
Matches 272; Conservative 55; Mismatches 78; Indels 0; Gaps 0;				
Qy	33 KKVAILTAGGLAPCLNSAIGSLIERETLDPISLILCYRGYKGLLGDSYPYAVARRK 92			
Db	3 KTVALLTAGGLAPCLNSAIGSLIERETLDPISLILCYRGYKGLLGDSYPYAVARRK 92			
Qy	93 AGTLQRFSGSVIGNSRYKLTNYVDCKRGIVYGEGBPQKRAAPQKDDGDIILATIGDD 152			
Db	63 AAVLHTVGSGLIGNSRYKLTNYVDCKRGIVYGEGBPQKRAAPQKDDGDIILATIGDD 122			
Qy	153 TTTAAADLAFLAFLRNRYGLTVIGLPTVNDVDFPIKQSLGAWTAAGARYPFNVVAENN 212			

Db	123	TNTAAADLAAYUKASRGYTLFRVIGLPTINDIIVPRLQSLGAMTAQAQSRFFQVVAEQT	1822
Qy	213	ANPRMLITHEWMOGRNCGHLLTAATAOEYRLUDRAWELELGITRESEVPAVYPSKALTD	2722
Db	183	ANPRVLLVHEWVGRSGCYLLPQAAADYRQQLNHRFPALGHTERRRDYTHAAVVEPTID	2422
Qy	273	LEBAKCLREVMKXVDCVNI FVSEBGAVEBAIYAEMOAKQOEVPBPAFGHILKLDVANGXW	3322
Db	243	LKBAARLRAWMRVOCVNI FLSEBGGINDIVIAEMTATAGEVTPBDFPFGHVIDIDLINGAW	3020
Qy	333	FGSQPAMTIAEAKTLYVQSGYFPAPASAVNDMRLIKSCADLAVECAFPRRSGVTGDED	3922
Db	303	FGSQPFGMWADKYLIVQSGYFSRSRSPANAEDRLRIKGMVDLADCAIRGASGLIGDDE	3622
Qy	393	NGVULALIEPRRIKQKQFPNIDTDPMNSLSTLGQPKRGKYEVS	437
Db	363	RNGVULALIEPRKQKQAFNIDHPMTHLNLTGQPKAKQSVAH	407

RESULT 2	092NM9	PRELIMINARY:	PRT:	404 AA.
ID	092NM9			
AC	Q92NM9;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Probable pyrophosphatase--fructose 6-phosphate 1-phosphotransferase			
DE	protein (EC 2.7.1.90).			
GN	PFK OR R02190 OR SMC01862.			
OS	Rhizobium meliloti (Sinorhizobium meliloti).			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC	Rhizobiaceae; Sinorhizobium.			
OX	NCBI_TaxId=382;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1021;			
RA	MEDLINE=21396507; PubMed=11481430;			
RA	Capela D., Barloy-Hubler F., Gouzy J., Bothé G., Ampe F., Batut J			
RA	Boisard P., Becker A., Boutry M., Cadieu E., Dreno S., Gloux S.			
RA	Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,			
RA	Renard C., Portecaille D., Puhler A., Purnelle B., Ransperger U.,			
RA	Paul C., Theault P., Vanderbol M., Weidner S., Gallbert F.;			
RT	"Analysis of the chromosome sequence of the legume symbiont			
RT	Sinorhizobium meliloti strain 1021."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).			
DR	EMBL: AL591789; CAC4766.1;			
DR	InterPro: IPR000023; Pfctnckinase.			
DR	Pfam: PF00365; PFK, 1.			
DR	PRINTS: PR00476; PHPFCTKINASE.			
DR	Prodom: ED000707; Ppfctnckinase; 1.			
DR	Transferase; Complete proteome.			
DR	STOUCNCR 404 AA; 43712 KW; 16E5ECD966AA13D5 CRC64;			

Query Match	57.0%;	Score 1302;	DB 16	Length 404;
Best Local Similarity	62.3%;	Pred. No. 4.2e-89;		
Matches 246;	Conservative 59;	Mismatches 90;	Indels 0;	Gaps 0;
QY	KKVAITTAGAGLAPCNSAIGSLIEREYTEIDDSIRIICRGSGYGLLGDSPYTLAEVRKK	92		
Db	KKVAMTLKAGLAPCGLSSAVGSLIEREYTDLADYELVAVRSGYGLLADRIETTPMRKK	63		
QY	AGLQRFSGSGVSGNSRVELTLYWYKDCYKRGVYKEEPPQKAAAOYLKMGDILHRTGGD	152		
Db	AYLHRHGGSGPLGNSRVELTMTADCYKRGVYKEEENLPRFAERLLASDGLSLHTGGD	123		
QY	TTTTAAADLAFLARNNYGLTYIGLPKTYDNDVPFIKSLGAWTAAGAGAFYEMTVAAENN	212		
Db	TTTTAADLAAITAGAGNGYDITLVGGPKTYDNDVVFIRGLTAAWTAAGAFPDHVSNEOS	183		
QY	ANPRMLIVHEVMGRNCGMLTAATAQCYRKLDDRAEMLPBELGLTRESSEYHAFAVFPMAID	272		
Db	AAEPTLVVHEVMGRRCGMILTAATAAYTHLAGNKEYVDGEMMAAQNINDIGLYPEMAFD	243		

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0Y 277 LEEAEKRLBEMDXVCVNI FVSSEAGVEALIAEMQAGSEVPDPAFGHITLDAVNGKM 3323
Db 244 LEEBAARLBEMVDRAFPVTL FVSEBACIDDAIAEBEAGAEVTKCDPAFHVNIIDITINGNM 3030
0Y 333 FGEOPAMIOGAEKTLVOKSGYPARASASNVDDMLIKSCADLAVECAFRESGVTGHDED 3923
Db 304 FSKQFPALLGAERBSKVSQSGYIARSAIPANVDDRLIGSMVDLAVESALINKVSGVTGHDED 3653
0Y 393 NGNVLRALIEFPRIKGGKCPENIDTDMVFNMSLEBIG 427
Db 364 QGGRALTIEFPRIKGGKHEDTSAKKFGEMVYVG 398

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RESULT 3		
Q8UDL0		
ID	Q8UDL0	PRELIMINARY; PRT; 514 AA.
AC	Q8UDL0;	
DT	01-JUN-2002 (TREMBLrel. 21, Created)	
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DE	Pyrophosphate-fructose-6-phosphate 1-phosphotransferase.	
GN	Pfp OR AtU2115 OR ACP_C_3836.	
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).	
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;	
OC	Rhizobiaceae; Rhizobium.	
OX	NCBI_Textid=176299;	

RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monke D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
 RA Chen Y., Paulsen I.F., Eichen J.K., Katz P.D., Boyee D., Str,
 RA Chapman P., Cledenning J., Deatherage G., Giller W., Grant C.,
 RA Kutlayin T., Levy R., Li M.-Y., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saepthimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tiao L., Biddle P., Jung M., Krespan V., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neeter E.W.;
 RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
 RT C58."
 RL Science 294:12317-2323(2001).
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194; Miller N., Blanchard M.,
 RA Goodner B., Hinkle G., Gattung S.,
 RA Courjoll B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaudin M., Iatchouk O., Bpp A., Liu F.,
 RA Mollan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
 RA Cleo C., Slater S.;
 RT "genome sequence of the plant pathogen and biotechnology agent
 RT *Agrobacterium tumefaciens* C58."
 RL Science 294:2323-2328(2001).
 DR EMBL: AB009161; AML43105.1; ALT _INTT.
 DR EMBL: AB008127; A3K87863.1; -_-_-
 DR JntefPro: JPR000023; Pfrncknase.
 DR Pfam: PF00385; PFK_1.
 DR PRINTS: PR00476; Pfrncktnase.
 DR ProDom: PD000707; Pfrncktnase; 1.
 DR Trnasease; Complete proteome.
 QM SEQUENCE 514 AA; 55841 MW; B92DF77E39F0E0AD Crc64;

Query Match	56.6%	Score 1292.5	DI 16	Length 514
Best Local Similarity	57.9%	Pred. No. 3.1e-87		
Matches 246	Conservative 7	Mismatches 10	Indels 7	Gaps 2
QY	8	HLTPADI--- <td>63</td> <td></td>	63	
Db	89	HLHAAVASISQITCLWYAK--RRANNAKKQKVALITNGSLADCLNSAIGSLIERYSIDLP	145	
QY	64	SIILITCRGGKSHLLDSYPTVAEYKKKGQVQRFQGSYVIGNSRVTLTWKDCCKEGLV	123	

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146 EIDIIATSGYGVILGRIETITKMKRAHLIRHYGSPIGNSRVKTITNADACAKGLV 205
124 KEGEDPOKVAADOLVKQGVDIHTITIGDDITTAADLAFLARNYGLTVGLPKTVND 183
206 KEGNDPLVAERLAADGITITHTIGDDITTAADLAAYIGANGYDLTVGLPKTVND 265
184 VPIIKOSIGANTAAEQARFYMTVAENANPRLIYHEWGNCGMLTAATQERYELL 243
266 VPIIKOSIGANTAAEQARFYMTVAENANPRLIYHEWGNCGMLTAATQERYELL 325
244 DRAEMPELIGLTSRYEVAHFEMAIIDLBAEKRLREVWDXDQCNITFVSBAGYEA 303
326 RGNVYVEGLMNTOMKINDIGIYDPMADIEAEERLKEVMDKGYVTLTVSBSAGLDA 385
304 VAENQAGQEVPRDAFGHILKDAVNPGRKEGEPQOMIGAKTLVQKGYFARASAVND 363
386 VAERBAAGEAVKRDAPFGVKIDITLVGGMFQKOPAGLIGERSWVQSGYFARASAPAND 445
364 DMRLIXSCADLAVECAFRESGVIGHEDNGENVRAIEFRIKSGKFPNIDTWFNSML 423
446 DLRLIQGVNDLAESALNKVSGVGHEDDQNGKLRITIEPRIKSGKFPNIDTWFNSML 505
424 EIGQP 428
506 HWGP 510

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RESULT 4

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Q9KH71 PRELIMINARY; PRT; 346 AA.
ID Q9KH71;
AC Q9KH71;
DT 01-OCT-2000 (TREMblrel, 15, Created)
DT 01-OCT-2000 (TREMblrel, 15, last sequence update)
DT 01-JUN-2002 (TREMblrel, 21, last annotation update)
DE Ppi-dependent phosphofructokinase.
GN PPI.
OS Dictyoglomus thermophilum.
OC Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
OX NCBI_TaxID=14;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL46 B.1;
RX MEDLINE=20372656; PubMed=10913106;
RA Ding Y.-H.R., Ronimus R.S., Morgan H.W.;
RT "sequencing, cloning, and high-level expression of the pfr gene,
thermophilic eubacterium Dictyoglomus thermophilum."
RL J. Bacteriol. 182:4661-4666(2000).
DR HSP; AP268276; AAF80100.1; -.
DR HSP; P06998; 2PFK.
DR InterPro: IPR000023; PfrnucKinase.
DR Pfam: PF00365; PFK.1
DR PRINTS; PR00476; PFRCTKINASE.
DR ProDom; PD000707; PfrnucKinase; 1.
KW Kinase.
SQ SEQUENCE 346 AA; 37448 MW; 50C03B64BA7927F1 CRC64;

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Query Match 13.4%; Score 305; DB 2; Length 346;
Best Local Similarity 27.5%; Pred. No. 2, 2e-14;
Matches 107; Conservative 73; Mismatches 155; Indels 54; Gaps 15;
QY 34 KVALITAGLAPCLNSAIGSLIERYTEIDPSIEIICTRGYKGLLIGDSYPTVAERKKA 93
DB 5 RIVGLVGGGCPGLNPAIRGIYMR--ALDYGEVIGLKYGMAGLLKADTMPISLEVED- 61
QY 94 GVLQRRGSGVIGNSRVKLTNVNDCVARGLVKGEDEPOKVAADOLVKQGVDIHTIGDDT 153
DB 62 --ILBGGITLSSR---TNP-----FKGEEDVQK--CVENFKLINDALIAIGGSJT 107
QY 154 NTAADLAFLARNYGLTVIGLPTVNDVFPPIKOSIGANTAAEQARFYMTVAENAN 213
DB 108 LSVASRF-----SKGLPMIVGPKTIDKLBETDVTIGPDVAEYVVVAIKRLDTAS 161

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QY 214 NPRLIYHEWGNCGMLTAATQERYKLLDRABMLPEIGLTSRYEVAHFEMAIIDL 273
DB 162 HAVIVV-ELMGNHAGMLL-----YGLAGADY-----ILIPVEPNL 200
QY 274 EAEKRLREVWDX-VDCWNI FVSEAGVEAIYAEOMKQGEVPRDAFGHILKDAVNGK 332
DB 201 EDLYNRIKLYAGRNRHVAVALAEVQLPEFTYO---KQEGNVDAFGHILGCV--GNV 255
QY 333 FGEOPQMIGAKTLVQKGYFARASAVNDMLIKSCADLAVECAFRESGVIGHED 392
DB 256 LAEIQKTLGIERAVYILS-HLQGGSPSTRDKIMKLLQKAVDLVHBSKSLF--VAV 312
QY 393 NGNVLAIEFPRIKSGKFPNIDTWFNSM 421
DB 313 KGNELVPDITLIE-GTKNVDPAFYESV 340

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RESULT 5

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Q9FJ05 PRELIMINARY; PRT; 488 AA.
ID Q9FJ05;
AC Q9FJ05;
DT 01-MAR-2001 (TREMblrel, 16, Created)
DT 01-MAR-2001 (TREMblrel, 16, last sequence update)
DT 01-JUN-2002 (TREMblrel, 21, last annotation update)
DE Pyrophosphate-dependent phosphofructo-1-kinase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=98403884; PubMed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Physically assigned P1 and TAC clones."
RL DNA Res. 5:203-216(1998).
DR EMBL; AB013392; BAB09881.1; -.
DR HSP; P00512; 3PFK.
DR InterPro: IPR000023; PfrnucKinase.
DR Pfam: PF00365; PFK.1
DR PRINTS; PR00476; PFRCTKINASE.
DR ProDom; PD000707; PfrnucKinase; 1.
KW Kinase.
SQ SEQUENCE 488 AA; 53781 MW; ABA526AED9213B17 CRC64;

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Query Match 12.3%; Score 282; DB 10; Length 488;
Best Local Similarity 26.8%; Pred. No. 1, 9e-12;
Matches 112; Conservative 60; Mismatches 156; Indels 86; Gaps 18;
QY 37 ILTAGLAPCLNSAIGSL-----IERYTEIDPSIEIICTRGYKGLLIGDSYPTVA 87
DB 96 IYTCGGLGGLNTVIREVSSLSYKGVKRLIGDIVSL-----CGYGFVAKNTIPLMS 149
QY 88 EYKKAAGLQRRGSGVIGNSRVKLTNVNDCVARGLVKGEDEPOKVAADOLVKQGVDIHT 147
DB 150 KV--VNDIHRGGGITITSR-----GSHDTNKK--VDSIQGRGINQYVT 189
QY 148 IGGDDTNTAAADLAFLARNYGLTVIGLPTVNDVFPPIKOSIGANTAAEQARFY--M 205
DB 190 IGGDGTQAGASVTFEIRRRRLKXAVVGIIPTINDIDVIDIKSPGPDVAEBAQAINDA 249
QY 206 NVVANNANPRLIYHEWGNCGMLTAATQERYKLLDRABMLPEIGLTSRYEVAHF 265
DB 250 HVEAESNNGIGLV--KLMGYSGYIA-----WYATLASRDVDCCL 288
QY 266 VPEVAIDLEAFA-----KRLREVWDXVCNITFVSEAGVEAIYAEOMKQGEVPRDA 318
DB 289 IPESFYIAGGGGLFPIERLRLKHGHNV-----IYLAAGAGQDLAKMSNES-----TPVDA 340

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QY 319 FGHKIDAVNPGKFEQFOAQMIGAETIVQ---KSGTPARASASVNDMLIKSCADL 374
 DB 341 SGRKLLKDV--GLMISQSIKDHFKKRWNNLKYIDPTWIRAPSVASDNVCTLLAQSAVHAM 398
 QY 375 AVACAFRRSGVGHDED--NGNVLAIEPRRIKGGKPPNIDD--WNSMLSEIQP 428
 DB 399 AVHGA---AGTYGYSGLVNGR-QTYIPRYRITETQNNVITDRMKAR-LLSTNQP 451

RESULT 6

Q9C5J7 PRELIMINARY; PRT; 485 AA.

ID Q9C5J7
 AC Q9C5J7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative pyrophosphate-dependent phosphofructo-1-kinase.
 GN MK19.8/AT5G56630.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.D., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shimizu P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Full length cDNA of gene MK19.8/AT5G56630 (GI:10176767).";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
 RA Quach H.D., Tang C., Toriumi M., Yu G., Bowser L., Carninci P.,
 RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shimizu P., Southwick A., Tracy S.E.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene MK19.8/AT5G56630 (GI:10176767).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A7360207; AAK25917.1; -;
 DR EMBL: AY040055; AAK64113.1; -;
 DR HSSP: P00512; 3PK;
 DR InterPro: IPR000023; Pfpruckinase.
 DR Pfam: PF00365; PFK; 1.
 DR PRINTS: PR00476; PPRCKINASE.
 DR ProDom: PD000707; Pfpruckinase; 1.
 DR KINASE
 SQ SEQUENCE 485 AA; 53482 MW; 6P0C6CF43BA7B5 CRC64;

Query Match 12.3%; Score 281.5; DB 10; Length 485;
 Best Local Similarity 26.7%; Pred. No. 2e-12;
 Matches 109; Conservative 61; Mismatches 166; Indels 73; Gaps 16;

QY 37 ILTAGLACNSAIGSLERTEIDPSIEIICRYGGYKGLLGSYPYTAVERKKAQVL 96
 DB 96 IYTCGLCGNLTVAREVSSLSYMGVRRILGIDGTRGFYAKTTIPLNSRY--VNDI 152
 QY 97 QRFSGSVIGNSRVKLTNVDCVKGIVKEGDEPOKVAADQVLKVDGVDILHTIGGDDITTA 156
 DB 153 HRRGGTITGSR-----GHDITNMI-VDSIDRGINQVYIIGGGCTGRG 195
 QY 157 AADLAFLARNNYGLTVIGLPTVNDVFPFKISGARTAAEQGARF--NAVVAENAN 214
 DB 156 ASVIEIRRLKVAVVGIIPTIINDLPVIDISFGFTVAVEAQRALNAHVEAESMEN 255

QY 215 PMHIVHEWGRNGMTLTAATQERYKLDRAEMLPELGLTRESYEVHAFVPEMAIDLE 274
 DB 256 GIGFV--KLNGRYGYIA-----WYATIASRDVDCCLIPSPFYLE 294
 QY 275 AEA-----RLEPMVKDCVNI FVSEAGVAEIVAMQAGQVEPRDAFGHKIDAV 327
 DB 295 GEGGLFETIERKLDDHGMV---IYLAEGAGQDMCKMSNES---TPMDSGNKLLKDV 346
 QY 328 NPGKWFGEQFOAQMIGAETIVQ---KSGTPARASASVNDMLIKSCADLAVECAFRE 383
 DB 347 --GLMISQSIKDHFKKRWNNLKYIDPTWIRAPSVASDNVCTLLAQSAVHAM--- 401
 QY 384 SGVIGHSD--NGNVLAIEPRRIKGGKPPNIDD--WNSMLSEIQP 428
 DB 402 AGTYGYSGLVNGR-QTYIPRYRITETQNNVITDRMKAR-LLSTNQP 448

RESULT 7

Q9XL57 PRELIMINARY; PRT; 366 AA.

ID Q9XL57
 AC Q9XL57;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 6-phosphofructokinase.
 GN PFK OR CPT185.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STAIN-13 / Type A;
 RX PubMed:11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori W., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
 DR EMBL: AP003189; BAB80891.1; -;
 DR InterPro: IPR000023; Pfpruckinase.
 DR Pfam: PF00365; PFK; 1.
 DR PRINTS: PR00476; PPRCKINASE.
 DR ProDom: PD000707; Pfpruckinase; 1.
 DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 1.
 DR KINASE
 SQ SEQUENCE 366 AA; 39514 MW; C5614C41A638C31 CRC64;

Query Match 12.2%; Score 278; DB 16; Length 366;
 Best Local Similarity 26.2%; Pred. No. 2.4e-12;
 Matches 113; Conservative 67; Mismatches 127; Indels 124; Gaps 20;

QY 28 IANKPKVAIITAGLAPCNSAIGSLERTEIDPSIEIICRYGGYKGLLGSYPYTA 87
 DB 1 MMQPIKILKILITGGDDCGMLNAVIRA-VTETALIKYEVYIIGYRGGLYNDF--VKL 57
 QY 88 EVRRKAGVLOFGSGVIGNS-----RYKLTNVKDCVKGIVKEGDEPOKVAADQVLK 139
 DB 58 DLDVSGLIHR-GSTILHSSKNKDLFDYQVDENGK-----IYK-KDVSVDVENLKK 108
 QY 140 DQVDIILITGGDDPNTAAADLAFLARNNGYLVYIGLPTVNDVFPFKISGARTAAEQ 199
 DB 109 EGVVALVVGDDGLTISARP-----SRKGVNIVGPKTIINDLTLTVDFPGNTATEI 162
 QY 200 GARFANVAVENNANPMLIVHEWGRNGMTLTAATQERYKLDRAEMLPELGLTRESY 259
 DB 163 ATBALDRLHTAABSHHIMKL-EVGRNAGTIAL-----ESGIAASA- 203
 QY 260 EVHAFVPEPAIDLE--ABAQRLEPVNDKDCVNI FVSEGA---GVRAIYAEQAKQGV 314
 DB 204 --DVILLPEIPYDINKIVKEREEREGKQFTI-IYVAEAKRPDGGVVS-----KI 253
 QY 315 PDAFGHKIDAVNPGKFEQFOAQMIGAETIVQSGYFAPARASASVNDMLIKSCADL 374

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Db      254 VMDSPDRLGCI-----ANKLAIDLG-----LTKN----- 280
QY      375 AVECAFRESGVIGHDENGNV-----LRAIEPRKIGKGFNIIDTWNFNSKL 422
Db      281 -----HEIRSTVLGHIOGANTSTYDRILSTKYGVKAVEL-----INSNLFGNNV 325
QY      423 SEIGQPKGVK 433
Db      326 A-----LKNKV 332

RESULT 8
ID 09AGC0 PRELIMINARY; PRT; 341 AA.
AC 09AGC0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Phosphofructokinase-1 like protein (EC 2.7.1.11) (6-phosphofructokinase)
DE (phosphohexokinase).
OS Amycolatopsis mediterranei (Nocardia mediterranei).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=33910;
RN SEQUENCE FROM N.A.
RC STRAIN=5659;
RA Kuan L., Mueller M., August P.R., Pogoseva-Asadjanan E., Flores H.G.,
RA Yu T.;
RT "Characterization and cloning of three 3-deoxy D-arabinoseputulosonate
RT 7-phosphate synthase isoenzymes from Amycolatopsis mediterranei
RT 5659."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-
CC -1- FRUCTOSE 1,6-BISPHOSPHATE.
CC -1- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
CC EMBL; AF36847; AACZ8147.1; -.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR000023; Pfrtuckinase.
DR Pfam; PF00365; PFK.1
DR PRINTS; PR00476; PFRCTKINASE.
DR PRODOM; PD000707; Pfrtuckinase.1.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE.1.
DR GLYCOLYSIS; Kinase; Transferase.
KW SEQUENCE 341 AA; 36272 MW; 285C28E7BD57065 CRC64;

Query Match 12.0%; Score 274.5; DB 2; Length 341;
Best Local Similarity 26.8%; Pred. No. 3.9e-12;
Matches 101; Conservative 60; Mismatches 151; Indels 65; Gaps 15;

QY      34 KVALITAGLAPCLNSAIGSLIERYTEIDPSIRIICYRGYKGLLGDSPVTAVERKKA 93
Db      2 RGVVLGGGCGPCPLNVIKAVKGEIVH-GMDFVGRGNMCPFLGDSRPL-GLNDVE 58
QY      94 GYLORFGGSVIGNSRYKLTNNKDCYKRGVKEGEDPQVAAQDLVKGVDILHTIGSDT 153
Db      59 DILTR-GGITLRSSRTNRYVEGVGDK--IKQ-----VLADQ-----GVDALITIGSDT 105
QY      154 NTAADLAFLAANNYGLTVIGLPTVNDVDFPIKOSLGAMTAAGAGAYFNVVAENNA 213
Db      106 LGVAKKL-----TDDIGVGVKTIINDLGAITDFTGPTAVSATAIDELHTTAAS 159
QY      214 NPKMLIVHEVWGNCGMLTAATAGQEVKCLDRAEWLPELGLTRESYEVAVFVEMALDL 273
Db      160 HRAALIV-EVWGNHAGMIALHS-----GLAGCA-----SVILVPEHFNIV 198
QY      274 EAARARLRVMDKVDVNIIVFVSEGAVGEAVIABMOKGQEV---RDAFGHILKIDAVNP 325
Db      199 DQVSWVERREFEAPFPIIVAGALPEG-----GEKKLTGKDAFGVRLGGI-- 248
QY      330 GKAFGQOPAMIGAEKTLVQKSGYFARASAVNDVDELTKSCADLAVEGAFRESGVIGH 389

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Db      249 GTWLADELHARTGKESRAV-VLGHVQKGTPTAHYRVATATRGILANVADADGFCWM-- 305
QY      390 DEBNGNVLAIEFPRIK 406
Db      306 -----VALKGTDIVRYK 317

RESULT 9
ID 051669 PRELIMINARY; PRT; 448 AA.
AC 051669;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (PFK).
DE BB0727.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gunn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M.,
RA Peterson U., Keriavage A.R., Quackenbush J., Salzberg S., Wainman J.,
RA Ullrichback T., Watthey L., McDonald L., Artlich P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith R.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi".
RL Nature 390:580-586 (1997).
DR EMBL; AE001172; AAC67070.1; -.
DR HSSP; P00512; 3PFK.
DR TIGR; BB0727; -.
DR InterPro; IPR000023; Pfrtuckinase.
DR Pfam; PF00365; PFK.1.
DR PRINTS; PR00476; PFRCTKINASE.
DR PRODOM; PD000707; Pfrtuckinase.1.
DR TRANSFERASE; Complete Proteome.
KW SEQUENCE 448 AA; 49887 MW; A4BA292360032D51 CRC64;

Query Match 11.8%; Score 270; DB 16; Length 448;
Best Local Similarity 24.9%; Pred. No. 1.3e-11;
Matches 102; Conservative 69; Mismatches 177; Indels 62; Gaps 11;

QY      34 KVALITAGLAPCLNSAIGSLIERYTEIDPSIRIICYRGYKGLLGDSPVTAVERKKA 93
Db      81 KVALITCGGCGPFDVRSIVRTLMKIYGVANIYGVKGGGLPESNSPFINNPV 140
QY      94 GYLORFGGSVIGNSRYKLTNNKDCYKRGVKEGEDPQVAAQDLVKGVDILHTIGSDT 153
Db      141 DDINFGGTLIGSS-----RGKIPV-----IYDTERMINIMINIFNIGSGGT 183
QY      154 NTAADLAFLAANNYGLTVIGLPTVNDVDFPIKOSLGAMTAAGAGAYFNVVAENNA 213
Db      164 QKGSLLIABEIERKRLKAVVGIPTVNDVDFPIKOSLGAGAYFNVVAENNA 243
QY      214 NPKMLIVHEVWGNCGMLTAATAGQEVKCLDRAEWLPELGLTRESYEVAVFVEMALDL 273
Db      244 AVNGIGLVKMGROSGFIAAHTA-----LSSNDVFCILPELDPI 284
QY      274 EAE-----AKEL-REVMKVDVNIIVFVSEGAVGEAVIABMOKGQEV---RDAFGHIL 322
Db      285 EGPNGFVHLERRILKESLIERIHAVALIABAG-----OKTFPHFKKDDSGNL 336
QY      333 KLDVAVPKMFGQBOAQMTGAEK--TLVQ-KSGYFARASAVNDVDELTKSCADLAVEC 378
Db      337 LYEDI--GLVTKDKITEYKAKNIQFTLKYIDPSYIIRSSPANAADSISYCARLASNAVHA 394
QY      379 AFRESGVIGHDEBQGNVLAIEFPRIKIGKGFNIIDTWNFNSMLSEIQP 428

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Db 395 AAGAKTMLISLWSTKFEVPIKAVIQRN-VNNGSFWMDVLSSTQOP 443

RESULT 10

ID 094AA4 PRELIMINARY; PRT: 489 AA.

AC 094AA4: 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE AT4926270/T25K17.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC OC Brasicales; Brassicaceae; Arabidopsis.
 OX NCB:TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bower L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai U., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RA "Arabidopsis cDNA clones";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,
 RA Bower L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai U., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RA "Arabidopsis ORF clones";
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP EMBL: AY049245; AK83587.1; -
 DR EMBL: AY090267; AAL90928.1; -
 DR InterPro: IPR000023; Pfriuckinase.
 DR Pfam: PF00365; PFK; 1.
 DR PRINTS: PR00476; PFRCTKINASE.
 DR PRODOM: PD000707; Pfriuckinase; 1.
 DR PRODOM: PD000707; Pfriuckinase; 1.
 SO SEQUENCE 489 AA; 53666 MW; A82C1EAI5B64F7B0 CRC64;

Query Match 11.6%; Score 266; DB 10; Length 489;

Best Local Similarity 25.7%; Pred. No. 2.9e-11;

Matches 105; Conservative 61; Mismatches 172; Indels 70; Gaps 13;

QY 37 ILTAGLAPCLNAGSLIRRYTEIDPSIILCYRGYKGLLDSDSYVTAFAVKKXGVL 96
 DB 96 IVFCGGLCPGLNVTREIVSLSVYGVKRLIGIDGGRGYAKNTVSLDSKVA--VNDI 152
 QY 97 QRFSGSVIGNSRVKLTNYKDCVKGKLVKGEEDPQKVAADQLVKQGVDTLHTIGDDTNTA 156
 DB 153 HKRGDTILGTSR-----GHDITKRL-VDSIQDRIQNGVYIIGDDGORG 195
 QY 157 AADLAFLAARNNGELTVIGLPTVDNDVFPFKOSIGAMTAEGAKRFPMNVAVENANPR 216
 DB 196 ASVIFEEIRRGRLKAVAVIGIPKTIIDNDIPVIDKSGFPTAVEAEQPAIINAHAESIEIN 255
 QY 217 MLIVHEVGRNCGMLTAATAOEVRKLDRAEMLPBELGLTRESYEVHAFVPEMAIDLEAE 276
 DB 256 GIGVYKLMKRGYSGLFA-----MATTASRVYDCCILPESFYIEGE 296
 QY 277 A-----KLRVWDKVDKCNITFVSGAGVEALVAENQAGQGVPRDAFGHITLDAVNP 329
 DB 297 GGLPEYIEKRLKESGHNV-----LVTAAGQDLMKSKMESW---TLXDASGNKILKDV-- 347

QY 330 GKPFGEQPAOMTGAETLVQ---KSGYFAPASASVNDWELLKSCADLAVECAFRESG 385
 DB 348 GLMWSQSIKDFHFNQKKVWMLKYIDPTYMIRAVPSNADSVYCYTLAQSAVHGAMGYTG 407
 QY 386 VIGHDEDNGNV---LRAIEPRIKGGRFNIDTD--WFNSMLSEIGOP 428
 DB 408 YI-----SGLVNGRQTYIPYRILTEKONHAYITDRMAR-LISSTNQP 449

RESULT 11

ID 027651 PRELIMINARY; PRT: 436 AA.

AC 027651: 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Pyrophosphate-fructose-6-phosphate 1-phosphotransferase
 DE (EC 2.7.1.90).
 GN Entamoeba histolytica.
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCB:TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLIN=96235172; PubMed=8645233;
 RA Bruchhaus I., Jacobs T., Denart M., Tannich E.;
 RA "Pyrophosphate-dependent phosphofructokinase of Entamoeba histolytica:
 RT molecular cloning, recombinant expression and inhibition by
 RT pyrophosphate analogues";
 RT Biochem. J. 316:57-63 (1996).
 DR EMBL: X82173; CA57659.1; -
 DR HSP: P00512; 3PEK.
 DR InterPro: IPR000023; Pfriuckinase.
 DR Pfam: PF00365; PFK; 1.
 DR PRINTS: PR00476; PFRCTKINASE.
 DR PRODOM: PD000707; Pfriuckinase; 1.
 DR TRANSFERASE.
 SO SEQUENCE 436 AA; 47571 MW; 1CECCFC05DC8D63 CRC64;

Query Match 11.5%; Score 263.5; DB 5; Length 436;

Best Local Similarity 26.3%; Pred. No. 3.7e-11;

Matches 108; Conservative 68; Mismatches 164; Indels 71; Gaps 16;

QY 34 KVALITAGLAPCLNAGSLIRRYTEIDPSIILCYRGYKGLLDSDSYVTAFAVKKXGVL 91
 DB 82 KVALITAGLAPCLNAGSLIRRYTEIDPSIILCYRGYKGLLDSDSYVTAFAVKKXGVL 139
 QY 92 KAGVLPFGSVIGNSRVKLTNYKDCVKGKLVKGEEDPQKVAADQLVKQGVDTLHTIGDD 151
 DB 140 VSDIHQKGSILGTSR-----GAQSPVMAQFLIDNNFNILFTLIGD 181
 QY 152 DITTAADLAFLAARNNGELTVIGLPTVDNDVFPFKOSIGAMTAEGAKRFPMNVAVENANPR 211
 DB 182 GLTAKGNAIKELRRKRPVTVIGIPKTIIDNDIPVIDKSGFPTAVEAEQPAIINAHAESIEIN 241
 QY 212 NANPRMLIVHEVGRNCGMLTAATAOEVRKLDRAEMLPBELGLTRESYEVHAFVPEMAI 271
 DB 242 KSARNNGIYRMLGRAGFIAL-----VASLANG-----DANVLIDIEDI 282
 QY 272 DL-----EAAKRLREVDNVYDQVNFVSGAGVEALVAENQAGQGVPRDAFGHITLDAVNP 326
 DB 283 PITQICEFQGR---IMSKGHV-IYVABGA-----LQOKRPDLGLDCKSKNILLHDS 333
 QY 327 VNEGKMGEGEPAOMTGAETLVQ---KSGYFAPASASVNDWELLKSCADLAVECAFRESG 384
 DB 334 INVLRISITFYKLSIIEHTIETVPSYMRISAPCSAADAHCMCLANAAVAVAMAGKT 393
 QY 385 G-VIGHDEDNGNV---LRAIEPRIKGGRFNIDTD--WFNSMLSEIGOP 429
 DB 394 GLVTCGHNNV---FVSPIDRTSYIK-----RVNDGELVYMWASIEEK 436

RESULT 12

094J12 PRELIMINARY; PRT; 586 AA.

ID 094J12
AC 094J12
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative pyrophosphate--fructose-6-phosphatet
DE Putative pyrophosphate--fructose-6-phosphatet
DE phosphotransferase)
GN P0638D12.7 OR OSUNB0021A09.21.
OS Oryza sativa (Rice), and
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriobacteriota; Oryzae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0638D12.7";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
RT clone: OSUNB0021A09.21";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002972; BAB55499.1; -
DR EMBL; AP003218; BAB89469.1; -
DR Gramene; Q94J12; -
DR InterPro; IPR000023; Pfufuckinase.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PHFCTKINASE.
DR PRODOM; PD000707; Pfufuckinase; 1.
DR TRANSFERASE.
KW SEQUENCE 586 AA; 64060 MW; 28DE4F800386A3 CRC64;

Query Match 11.5%; Score 263.5; DB 10; Length 586;
Best Local Similarity 26.2%; Pred. No. 5.9e-11;
Matches 96; Conservative 53; Mismatches 158; Indels 59; Gaps 9;

QY 34 KVAITAGGLAPCINSAIGSLIERTEIDSEIILICRGYKGLLDSDYPAVEYKKA 93
DB 189 KACIVTCGGLCPGINTVIRLVOSLSHMYVNDIFGIQNGYKGFYSNTYIPMP--KSV 245
QY 94 GVLORFEGSVTGNRSVKLTNVKDCVYKGLYKGBDPOKVAADQLVNDGVDIHTIGDDT 153
DB 246 NDHHRGGTVLIGTSR-----GGHDTGKI-VDMICRGINQVYIIGDDGT 288
QY 154 NTAADLAATLARNNGVLTIVGLPKTYNDVFPILKOSLGAMTAAGGARFMMVVAENNA 213
DB 289 QKARVETKIRRGKLVAVAPKTIIDNDIAVIDSGFDSVVEKQRIIDAAHVEASS 348
QY 214 NPMALLVHEVNGNCGMTAATAGQRYKLLDRAEWLPELGLITRESEYVNAVFPEMAID 273
DB 349 AENGIGVLMKRGYSPTA-----MYATLASRDVDCCLIESPFPFL 389
QY 274 EABA-----KLEBEMDVDCNIFVSEAGAVEAIVAEQAKGSEVPDAFGHIKLDVA 326
DB 390 EGSGGLFEYIEKRLKENNHV-----IVVREGAGQDILAKSIAAAD--IDSAGNLL-- 440
QY 327 VNPGRFGEGFAOMIGAETLVQ-----KSGYFARASASVNDWRLIKSCADILAVECAFRR 382
DB 441 LDVGLVLTIRIKYCKKKGKEMTIKIDPTVYMRALPSNASDNVYCTLLAHSALHGAAG 500
QY 383 ESGVIG 388
DB 501 YSFTVG 506

RESULT 13

Q91G72 PRELIMINARY; PRT; 775 AA.

ID Q91G72
AC Q91G72
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Putative pyrophosphate-dependent phosphofructo-1-kinase.
DE Putative pyrophosphate-dependent phosphofructo-1-kinase.
GN P0710E05.25 OR P0671B11.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriobacteriota; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. NIPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0710E05.25";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0671B11.1";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002743; BAA99438.1; -
DR EMBL; AP002746; BAA12686.1; -
DR HSP; P00512; 3PFK.
DR Gramene; Q91G72; -
DR InterPro; IPR000023; Pfufuckinase.
DR InterPro; IPR000634; S/T_denydrtse.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PHFCTKINASE.
DR PRODOM; PD000707; Pfufuckinase; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW KINASE.

QY 36 ALVTAGGLAPCINSAIGSLIERTEIDSEIILICRGYKGLLDSDYPAVEYKKA 95
DB 374 ALVTGGLCPGINTVIRLVOSLSHMYVNDIFGIQNGYKGFYSNTYIPMP--KSV 430
QY 96 LORFGSVTGNRSVKLTNVKDCVYKGLYKGBDPOKVAADQLVNDGVDIHTIGDDT 155
DB 431 IHKRGTVLIGTSR-----GGHDTGKI-VDSIKDGINQVYIIGDDGT 473
QY 156 AAADLAATLARNNGVLTIVGLPKTYNDVFPILKOSLGAMTAAGGARFMMVVAENNA 215
DB 474 GASVIFQEVRRERGLKCSVGVPKTIIDNDIQVDSKSGFPTAVEBQRAINAHVEASSAE 533
QY 216 RMLIVHEVNGNCGMTAATAGQRYKLLDRAEWLPELGLITRESEYVNAVFPEMAID 275
DB 534 NGIGVLMKRGYSPTA-----MYATLASRDVDCCLIESPFPFL 574
QY 276 EA-----KLEBEMDVDCNIFVSEAGAVEAIVAEQAKGSEVPDAFGHIKLDVA 328
DB 575 KGLLEFTEKRLKDNHNV-----IVVREGAGQDILAKSIAAAD--DASGNKLL--LD 625
QY 329 PGKWRFGEGFAOMIGAETLVQ-----VQSGYFARASASVNDWRLIKSCADILAVECAFRR 383
DB 626 VGLMLSQIKDKHFKKKRFPITTKITIDPTVYMRALPSNASDNVYCTLLAHSALHGAAG 682
QY 384 SGVIGHDEDNQNLRA--IEPPI--KGGKPPNIDTWNSMLSEIGOP 428
DB 683 AGYGFVAAPVNGRAVYIPFYRIKTEKQKVVITTRMMAR-VLCSTNQP 729

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RESULT 14
ID Q24812 PRELIMINARY; PRT; 382 AA.
AC Q24812;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE PPI-dependent phosphofructo-1-kinase (EC 2.7.1.90).
GN PFK.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95143279; PubMed=7841199;
RA Huang M., Altsch R.A., Chang K.P., Kemp R.G.;
RT "Cloning and sequencing a putative pyrophosphate-dependent
RT phosphofructokinase gene from Entamoeba histolytica.";
RL Biochim. Biophys. Acta 1260:215-217 (1995).
DR EMBL; U12513; AAA2671.1; -.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR000023; Pfrckinase.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PFRCKTKINASE.
DR ProDom; PD000707; Pfrckinase; 1.
DR Kinease; Transferase.
SQ SEQUENCE 382 AA; 41747 MW; 7ECCEBP37CD4F87B CRC64;

Query Match 11.4%; Score 260; DB 5; Length 382;
Best Local Similarity 26.7%; Pred. No. 5.5e-11;
Matches 99; Conservative 63; Mismatches 149; Indels 60; Gaps 14;

QY 34 KVALITAGLACLSAI--GSLIERTEIDPSIRHICRGYKLL--LGSYPTAAVR 90
DB 37 KVALITCGGLCPGLNNVIRGLVLTNRYHVN-NIPGLMWGEGLVPELSYQRLTPRI 94
QY 91 KZAGVLOPFGSGVIGNSRVKLTNVKDCVRGLVKEGEDPOKVAADQLVKDGVDLHTTIG 150
DB 95 --VSDIHQGGSIILGTSR-----GAQSPVMAQFLDNNNNILFTLGG 135
QY 151 DDTNTAAADLAFLARNYGLTVIGLPTVNDVPIKOSLGAMTAAGARFNNVAAE 210
DB 136 DDTLGAANAINKELRRKVPITVVGIPKTIIDNDICTSTFQFAVGLSGEAINAAVSE 195
QY 211 NNANRPMILVHVMGRNCGMLTAATAQERYKLLDBAEMLPBELGLTRSEYHAAVFPKMA 270
DB 196 AKSAGKIGCIIVLMGRDGFIL-----YASLANG-----DANVLILPEID 236
QY 271 IDL---EAAKRLBVDKDCVNI FVSEGAGVEAIVAEMQAKQEVPRDAFGHI--KLD 325
DB 237 IPITQICEFVGKR---IMSKGHV--IIVAEGA-----LONQPKOLDIGTKSGIILMD 287
QY 326 ANPQKMGEGFOAOMIGAETLVQ--KSGYFARASASVNDRLTKSGADLAVECAFRE 383
DB 288 SINYRDSITTKLKSLIGIEBHETIKFEVDPSYIMRSAPCSADAHFPCMLAANAIVAAWAK 347
QY 384 SG-VIGHDEDN 393
DB 348 TGLVICHNNHNN 358

RESULT 15
Q9STQ7 PRELIMINARY; PRT; 500 AA.
AC Q9STQ7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Pyrophosphate-dependent phosphofructo-1-kinase.
GN T25K17.80 OR A14G26270.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Beyan M., Koetler P., Entian K.-D., Bancroft I.,
RA Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049171; CAB38956.1; -.
DR EMBL; AL161564; CAB79482.1; -.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR000023; Pfrckinase.
DR Pfam; PF00365; PFK; 1.
DR PRINTS; PR00476; PFRCKTKINASE.
DR ProDom; PD000707; Pfrckinase; 1.
DR Kinease.
SQ SEQUENCE 500 AA; 55295 MW; A09DF850C905087 CRC64;

Query Match 11.3%; Score 257.5; DB 10; Length 500;
Best Local Similarity 25.6%; Pred. No. 1.3e-10;
Matches 109; Conservative 59; Mismatches 167; Indels 91; Gaps 16;

QY 37 ILTNGGLAPCLNSAIGSL-----ISRYTEIDPSIRHIC-----YRGYGL 78
DB 92 ILVTCGGLCPGLNNVIRGLVLTNRYHVN-NIPGLMWGEGLVPELSYQRLTPRI 148
QY 79 LGSYPTAAVRKKAAGVLOPFGSGVIGNSRVKLTNVKDCVRGLVKEGEDPOKVAADQLV 138
DB 149 AKNTVSLDSKV---VNDIHQGGSIILGTSR-----GHDITTKI--VDSIQ 168
QY 139 KQGVILHTTGGDDTNTAAADLAFLARNYGLTVIGLPTVNDVPIKOSLGAMTAAGAR 196
DB 189 DRGINQYIILIGDGTORAGAVIEEIRIRRGAKVAIVGIPKTIIDNDICTSTFQFAV 248
QY 199 OGARYFNNVVAENNANRPMILVHVMGRNCGMLTAATAQERYKLLDBAEMLPBELGLTR 256
DB 249 EAQRAITAAVAEASISTNGIGVAKMKRYSGFIA-----MYATLAS 289
QY 259 YEVAAVFPPEMAIDLEAA-----KRLREVNDKDCVNI FVSEGAGVEAIVAEMQAKG 311
DB 290 RDVDCCLIPSPFYLBSGGLFYEIEKRLRESGHV---LVIAEGAGCQDLSKSMESM- 344
QY 312 QEVPRDAFGHIKLDVAVPGKPRGQPMQMGAEKTLVQ--KSGYFARASASVNDRLTKSG 367
DB 345 --TLKQASGNKLLKDV--GLMSQSTIKDHFNQKQVNMELKTIPTTIRVPSNASDNY 400
QY 368 IKSCADLAVCAFRRESGVIGHDEDNQNV---LRAIEFPRIKQKPFNIDTD--WFNSML 422
DB 401 CTLAAGAAVGAAGAGYGYI-----SGLVNGRGQTYIPFYRITRKONHVITDRMMAR-LL 454
QY 423 SRIQOP 428
DB 455 SSTNQP 460

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Search completed: January 29, 2004, 14:37:55
 Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 14:37:58 ; Search time 39 Seconds
(Without alignments)
2328.635 Million cell updates/sec

Title: US-09-941-947a-2

Perfect score: 2284
Sequence: 1 DVTWTFYHLTADIRFCWTF.....FNSMLSEIGPKGKIVSH 437

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2284	100.0	437	10	US-09-934-868-6
3	2284	100.0	437	11	US-09-941-947a-2
4	2284	100.0	437	12	US-10-320-874-16
5	2284	100.0	437	16	US-10-320-924-16
6	659	28.9	184	12	US-10-369-493-14348
7	306.5	13.4	350	12	US-10-369-493-8108
8	294	12.9	342	15	US-10-156-761-13610
9	284.5	12.5	341	15	US-10-156-761-14652
10	269.5	11.8	341	15	US-10-156-761-10355
11	261	11.4	345	12	US-10-369-493-18261
12	253	11.1	319	12	US-10-369-493-2905
13	250.5	11.0	357	12	US-10-369-493-9669
14	246.5	10.8	987	12	US-10-369-493-21998
15	240.5	10.5	320	9	US-09-815-242-13785

16	239.5	10.5	318	12	US-10-369-493-9652	Sequence 9652, Ap
17	238.5	10.4	320	9	US-09-815-242-10422	Sequence 10422, A
18	238.5	10.4	320	12	US-10-369-493-23638	Sequence 23638, A
19	229.5	10.0	295	12	US-10-369-493-8855	Sequence 8855, Ap
20	227.5	10.0	449	12	US-10-369-493-8876	Sequence 8876, Ap
21	226.5	9.9	320	9	US-09-815-242-11721	Sequence 11721, A
22	224.5	9.8	334	12	US-10-369-493-515	Sequence 515, App
23	223.5	9.7	319	12	US-10-369-493-17399	Sequence 17399, A
24	222.5	9.7	322	9	US-09-815-242-5425	Sequence 5425, Ap
25	222.5	9.7	322	9	US-09-815-242-11619	Sequence 12619, A
26	222.5	9.7	322	9	US-09-815-242-12907	Sequence 12907, A
27	222.5	9.7	360	12	US-10-369-493-19198	Sequence 19198, A
28	222	9.7	322	12	US-10-369-493-10132	Sequence 10132, A
29	222	9.7	340	12	US-10-369-493-18431	Sequence 18431, A
30	221	9.7	335	9	US-09-815-242-11346	Sequence 13346, A
31	218.5	9.6	320	9	US-09-815-242-10649	Sequence 10649, A
32	215	9.4	321	12	US-10-369-493-21210	Sequence 21210, A
33	213.5	9.3	321	12	US-10-369-493-128	Sequence 128, App
34	213	9.3	321	12	US-10-369-493-479	Sequence 479, App
35	207	9.1	959	12	US-10-369-493-1903	Sequence 1903, App
36	202.5	8.9	321	9	US-09-815-242-11162	Sequence 11162, A
37	201.5	8.8	361	12	US-10-369-493-2625	Sequence 2625, Ap
38	201	8.8	343	9	US-09-887-054-2	Sequence 2, Appli
39	201	8.8	343	15	US-10-098-626-2	Sequence 2, Appli
40	201	8.8	357	10	US-09-738-626-4883	Sequence 4883, Ap
41	200	8.8	776	15	US-10-205-342-5	Sequence 5, Appli
42	198	8.7	419	12	US-10-369-493-2919	Sequence 2919, Ap
43	196	8.6	321	12	US-10-369-493-10434	Sequence 10434, Ap
44	196	8.6	828	12	US-10-369-493-6730	Sequence 6730, Ap
45	193	8.5	942	12	US-10-369-493-2497	Sequence 2497, Ap

ALIGNMENTS

RESULT 1
US-09-934-901-16
Sequence 16, Application US/0934901
Parent No. US20020110885A1
GENERAL INFORMATION:
APPLICANT: Kofas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: No. US20020110885A1, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENTRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: C1619 US NA
CURRENT APPLICATION NUMBER: US/09/934, 901
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,906
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 437
TYPE: PRT
ORGANISM: METHYLOMONAS SP.
US-09-934-901-16

Query Match	Similarity	Score	DB ID	Length	Matches	Pred. No.	Mismatches	Indels	Gaps
1	100.0%	2284	10	437	437	0	0	0	0
2	100.0%	2284	10	437	437	0	0	0	0
3	100.0%	2284	11	437	437	0	0	0	0
4	100.0%	2284	12	437	437	0	0	0	0
5	100.0%	2284	16	437	437	0	0	0	0
6	28.9	659	12	184	184	0	0	0	0
7	13.4	306.5	12	350	350	0	0	0	0
8	12.9	294	15	342	342	0	0	0	0
9	12.5	284.5	15	341	341	0	0	0	0
10	11.8	269.5	15	341	341	0	0	0	0
11	11.4	261	12	345	345	0	0	0	0
12	11.1	253	12	319	319	0	0	0	0
13	11.0	250.5	12	357	357	0	0	0	0
14	10.8	246.5	12	987	987	0	0	0	0
15	10.5	240.5	9	320	320	0	0	0	0

QY 181 DNDVFPYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 240
 DB 181 DNDVFPYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 240
 QY 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEBAKRLREVMDCVNI FVSEAGV 300
 DB 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEBAKRLREVMDCVNI FVSEAGV 300
 QY 301 EAIVAEMQAKQGEVPRDAPFGHITKIDAVNPGKMPGEOFAOMIGAEXTLVOKSGYFARASAS 360
 DB 301 EAIVAEMQAKQGEVPRDAPFGHITKIDAVNPGKMPGEOFAOMIGAEXTLVOKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRRSGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMENS 420
 DB 361 NVDDMRLLKSCADLAVECAFRRSGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMENS 420
 QY 421 MLESIGQPKGKVEVSH 437
 DB 421 MLESIGQPKGKVEVSH 437

RESULT 2

US-09-934-868-6
 / Sequence 6, Application US/09934868
 / Patent No. US20020137190A1
 / GENERAL INFORMATION:
 / APPLICANT: Kofias, Mattheos
 / APPLICANT: Odem, James M
 / APPLICANT: Schenzle, Andreas J
 / TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
 / FILE REFERENCE: C11596 US NA
 / CURRENT APPLICATION NUMBER: US/09/934, 868
 / PRIOR FILING DATE: 2001-08-22
 / PRIOR APPLICATION NUMBER: 60/229, 858
 / PRIOR FILING DATE: 2000-09-01
 / NUMBER OF SEQ ID NOS: 81
 / SOFTWARE: Microsoft Office 97
 / SEQ ID NO 6
 / LENGTH: 437
 / TYPE: PRT
 / ORGANISM: METHYLOMONAS SP.
 / US-09-934-868-6

Query Match 100.0%; Score 2284; DB 10; Length 437;

Best Local Similarity 100.0%; Pred. No. 1,4e-223; Indels 0; Gaps 0;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTWPFYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 60
 DB 1 DVTWPFYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 60
 QY 61 IDPSIEIICRYGGYKGLIGDSYPTAEVRKAGVLOFGGSVIGNSRVKLTNVDCVCR 120
 DB 61 IDPSIEIICRYGGYKGLIGDSYPTAEVRKAGVLOFGGSVIGNSRVKLTNVDCVCR 120
 QY 121 GLVXGEDPQKVAADQVLKGDVILHTIGGDDTNTAAADLAFLARNNYGLTVIGLPTV 180
 DB 121 GLVXGEDPQKVAADQVLKGDVILHTIGGDDTNTAAADLAFLARNNYGLTVIGLPTV 180
 QY 181 DNDVFPYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 240
 DB 181 DNDVFPYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 240
 QY 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEBAKRLREVMDCVNI FVSEAGV 300
 DB 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEBAKRLREVMDCVNI FVSEAGV 300
 QY 301 EAIVAEMQAKQGEVPRDAPFGHITKIDAVNPGKMPGEOFAOMIGAEXTLVOKSGYFARASAS 360
 DB 301 EAIVAEMQAKQGEVPRDAPFGHITKIDAVNPGKMPGEOFAOMIGAEXTLVOKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRRSGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMENS 420
 DB 361 NVDDMRLLKSCADLAVECAFRRSGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMENS 420

DB 361 NVDDMRLLKSCADLAVECAFRRSGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMENS 420
 QY 421 MLESIGQPKGKVEVSH 437
 DB 421 MLESIGQPKGKVEVSH 437

RESULT 3

US-09-941-947a-2
 / Sequence 2, Application US/09941947a
 / Publication No. US2003003528A1
 / GENERAL INFORMATION:
 / APPLICANT: Brzostowicz, Patricia C.
 / APPLICANT: Cheng, Qiong
 / APPLICANT: DiCosimo, Deana J.
 / APPLICANT: Kofias, Mattheos
 / APPLICANT: Miller, Edward S. Jr.
 / APPLICANT: Odem, J. Martin
 / APPLICANT: Picataggio, Steve
 / APPLICANT: Rouviere, Pierre E.
 / TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
 / FILE REFERENCE: C11903 US NA
 / CURRENT APPLICATION NUMBER: US/09/941,947a
 / PRIOR FILING DATE: 2001-09-01
 / PRIOR APPLICATION NUMBER: 60/229,907
 / PRIOR FILING DATE: 2000-09-01
 / PRIOR APPLICATION NUMBER: 60/229,858
 / PRIOR FILING DATE: 2000-09-01
 / NUMBER OF SEQ ID NOS: 60
 / SOFTWARE: Microsoft Office 97
 / SEQ ID NO 2
 / LENGTH: 437
 / TYPE: PRT
 / ORGANISM: Methylomonas 16a
 / US-09-941-947a-2

Query Match 100.0%; Score 2284; DB 11; Length 437;

Best Local Similarity 100.0%; Pred. No. 1,4e-223; Indels 0; Gaps 0;

Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVTWPFYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 60
 DB 1 DVTWPFYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 60
 QY 61 IDPSIEIICRYGGYKGLIGDSYPTAEVRKAGVLOFGGSVIGNSRVKLTNVDCVCR 120
 DB 61 IDPSIEIICRYGGYKGLIGDSYPTAEVRKAGVLOFGGSVIGNSRVKLTNVDCVCR 120
 QY 121 GLVXGEDPQKVAADQVLKGDVILHTIGGDDTNTAAADLAFLARNNYGLTVIGLPTV 180
 DB 121 GLVXGEDPQKVAADQVLKGDVILHTIGGDDTNTAAADLAFLARNNYGLTVIGLPTV 180
 QY 181 DNDVFPYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 240
 DB 181 DNDVFPYHLTADIRFCHEFLNPFYTLNKKPKKVALITAGGLAPCLNSAIGSLIERYTE 240
 QY 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEBAKRLREVMDCVNI FVSEAGV 300
 DB 241 KLDRAEWLPELGLTRESYEVHAFVPEMAIDLEBAKRLREVMDCVNI FVSEAGV 300
 QY 301 EAIVAEMQAKQGEVPRDAPFGHITKIDAVNPGKMPGEOFAOMIGAEXTLVOKSGYFARASAS 360
 DB 301 EAIVAEMQAKQGEVPRDAPFGHITKIDAVNPGKMPGEOFAOMIGAEXTLVOKSGYFARASAS 360
 QY 361 NVDDMRLLKSCADLAVECAFRRSGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMENS 420
 DB 361 NVDDMRLLKSCADLAVECAFRRSGVIGHDEDNQNVLAIEFPRIKGGKPPNIDTDMENS 420
 QY 421 MLESIGQPKGKVEVSH 437
 DB 421 MLESIGQPKGKVEVSH 437

RESULT 4
US-10-320-874-16
Sequence 16, Application US/10320874
Publication No. US20030138909A1
GENERAL INFORMATION:
APPLICANT: Koffas, Mattheos
APPLICANT: Odem, J. Martin
APPLICANT: No. US20030138909A1on, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: C13619 US NA
CURRENT APPLICATION NUMBER: US/10/320,874
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US/09/934,901
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,906
PRIOR FILING DATE: September 1, 2000
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 437
TYPE: PR1
ORGANISM: METHYLOMONAS SP.
US-10-320-874-16

Query Match 100.0%; Score 2284; DB 12; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.4e-223;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTWPHLTADIRFCMFLNPFYTLNKPCKVALITAGGLAPCLNSAIGSLIRYTE 60
DB 1 DVVTWPHLTADIRFCMFLNPFYTLNKPCKVALITAGGLAPCLNSAIGSLIRYTE 60
QY 61 IDPSIELICYRGYKGLLDGSDYPTAEVRKAGVLRFGGSVIGNSRVLTNVKDCVXR 120
DB 61 IDPSIELICYRGYKGLLDGSDYPTAEVRKAGVLRFGGSVIGNSRVLTNVKDCVXR 120
QY 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAALAFANNGGLTVIGLPTV 180
DB 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAALAFANNGGLTVIGLPTV 180
QY 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAALAFANNGGLTVIGLPTV 180
DB 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAALAFANNGGLTVIGLPTV 180
QY 181 DNDVPIKOSLGAMTAEGARFYMNVVAENNANPMLIVHEVMGNCGLTAATQCYR 240
DB 181 DNDVPIKOSLGAMTAEGARFYMNVVAENNANPMLIVHEVMGNCGLTAATQCYR 240
QY 241 KILDRAEMLPELGLTRESYEVAHVPEMAIDLEAKRLREYMDKVCNIFVSSGAGV 300
DB 241 KILDRAEMLPELGLTRESYEVAHVPEMAIDLEAKRLREYMDKVCNIFVSSGAGV 300
QY 301 EAIVAEMQAKGQEVPRDAFGHILKDAVNPCKMFGBOFQOMIGAEXTLVORSGYFARASAS 360
DB 301 EAIVAEMQAKGQEVPRDAFGHILKDAVNPCKMFGBOFQOMIGAEXTLVORSGYFARASAS 360
QY 361 NVDNMLIKSCADLAVECAFRESGVIGHEDNNGVTLRAIEPRIRKGRPFNIDTWFNS 420
DB 361 NVDNMLIKSCADLAVECAFRESGVIGHEDNNGVTLRAIEPRIRKGRPFNIDTWFNS 420
QY 421 MLESIQPKGKGVESH 437
DB 421 MLESIQPKGKGVESH 437

RESULT 5
US-10-320-924-16
Sequence 16, Application US/1036924
Publication No. US20030129721A1
GENERAL INFORMATION:
APPLICANT: Koffas, Mattheos
APPLICANT: Odem, J. Martin
APPLICANT: No. US20030129721A1on, Kelley C.
APPLICANT: Ye, Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: C13619 US NA
CURRENT APPLICATION NUMBER: US/10/320,924
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US/09/934,901
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,906
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 16
LENGTH: 437
TYPE: PR1
ORGANISM: METHYLOMONAS SP.
US-10-320-924-16

Query Match 100.0%; Score 2284; DB 16; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.4e-223;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVVTWPHLTADIRFCMFLNPFYTLNKPCKVALITAGGLAPCLNSAIGSLIRYTE 60
DB 1 DVVTWPHLTADIRFCMFLNPFYTLNKPCKVALITAGGLAPCLNSAIGSLIRYTE 60
QY 61 IDPSIELICYRGYKGLLDGSDYPTAEVRKAGVLRFGGSVIGNSRVLTNVKDCVXR 120
DB 61 IDPSIELICYRGYKGLLDGSDYPTAEVRKAGVLRFGGSVIGNSRVLTNVKDCVXR 120
QY 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAALAFANNGGLTVIGLPTV 180
DB 121 GLVGEEDPQKVAADQVLDGVDILHTIGDDTNTAAALAFANNGGLTVIGLPTV 180
QY 181 DNDVPIKOSLGAMTAEGARFYMNVVAENNANPMLIVHEVMGNCGLTAATQCYR 240
DB 181 DNDVPIKOSLGAMTAEGARFYMNVVAENNANPMLIVHEVMGNCGLTAATQCYR 240
QY 241 KILDRAEMLPELGLTRESYEVAHVPEMAIDLEAKRLREYMDKVCNIFVSSGAGV 300
DB 241 KILDRAEMLPELGLTRESYEVAHVPEMAIDLEAKRLREYMDKVCNIFVSSGAGV 300
QY 301 EAIVAEMQAKGQEVPRDAFGHILKDAVNPCKMFGBOFQOMIGAEXTLVORSGYFARASAS 360
DB 301 EAIVAEMQAKGQEVPRDAFGHILKDAVNPCKMFGBOFQOMIGAEXTLVORSGYFARASAS 360
QY 361 NVDNMLIKSCADLAVECAFRESGVIGHEDNNGVTLRAIEPRIRKGRPFNIDTWFNS 420
DB 361 NVDNMLIKSCADLAVECAFRESGVIGHEDNNGVTLRAIEPRIRKGRPFNIDTWFNS 420
QY 421 MLESIQPKGKGVESH 437
DB 421 MLESIQPKGKGVESH 437

RESULT 6
US-10-369-493-14348
Sequence 14348, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14348
LENGTH: 184
TYPE: PR1

ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14348

Query Match 28.9%; Score 659; DB 12; Length 184;
Best Local Similarity 67.9%; Pred. No. 1.1e-58;

Matches 125; Conservative 27; Mismatches 32; Indels 0; Gaps 0;

QY 33 KVALITAGGLAPCLNSAIGSLIERTEIDPSIBICRGYKGLLDDSPVTAVERKA 92
DB 1 QKVALITAGGLAPCLSSAAGSLIERYSIDIAVRSQVGLGEBIEITKDMERK 60
QY 93 AAVLRFSGSVIGNSRVKLTNVKDCVKGGLVEGEDPOKVAADOLVKQVDLHTTGDD 152
DB 61 AAILHRFGSSPIGNSRVKLTNVKDCVKGGLVEGEDPOKVAADOLVKQVDLHTTGDD 120
QY 153 TWTAAADLAFLARNNGYGLTVIGLPRYDNDVPPIKOSIGANTAAEGARFPMVAENN 212
DB 121 TWTAAADLAFLAAGANGYDLTVVGLPKTVNDVVPKOSIGANTAAEGARFPMVNSQS 180
QY 213 ANPR 216
DB 181 AAPK 184

RESULT 7

US-10-369-493-8108
Sequence 8108; Application US/10369493
Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 8108

LENGTH: 350

TYPE: PRP

ORGANISM: Thermobifida fusca

US-10-369-493-8108

Query Match 13.4%; Score 306.5; DB 12; Length 350;
Best Local Similarity 26.5%; Pred. No. 2.2e-22;

Matches 104; Conservative 63; Mismatches 145; Indels 81; Gaps 14;

QY 23 EFPYLTNNKPKKVALITAGGLAPCLNSAIGSLIERTEIDPSIBICRGYKGLLDD 82
DB 4 EFPYLTNNKPKKVALITAGGLAPCLNSAIGSLIERTEIDPSIBICRGYKGLLDD 58
QY 83 YPVTAVERKAGVLRFGGSVIGNSRVKLTNVKDCVKGGLVEGEDPOKVAADOLVKQV 142
DB 59 WPLDIEAVR--GILPR--GGTILGSSRTMLMKIEGVER-----VCDNMAALGV 103
QY 143 DILHTIGSDTNTAAADLAFLARNNGYGLTVIGLPRYDNDVPPIKOSIGANTAAEGAR 202
DB 104 DALVVAIGGEDTLGVARQL-----HDHGNNVGVPEKTINDLNDATDYFPGDTAVNATE 157
QY 203 YEMNVVAENNANPRMLIVHVRNGCMGLT-----AATQOEYRKLLDRAEMLPELGLTRE 257
DB 158 AIDRLHTTASHRRALV--EVMGRHAGMLALHAGMAAG-----195
QY 258 STEVNAVFPPEKALDIEBAKRLREVMKPYDCNIFVSGAGVEALVAMQAKQGVPRD 317
DB 196 ---NVLLTPEPFDIDEVAVVIESREKTNVAPITIVAGAPK---EGQLTLASARD 247
QY 318 AFGHKILDAVNGKMGFGQFQACMIGAEKTLVOKS---GYFAPASASNVDDMLIKSCADL 374

DB 248 SFGHVRIGI-----GQRLAEITEARTGEANSVLGHVORGSTPSAFPRVATRLGLH 301
QY 375 AVECAFRESGVIGHEDNGNV--LRAIEPPI 405
DB 302 AITAV-----HDKDFGMVALRGTETIVRV 325

RESULT 8

US-10-156-761-13610
Sequence 13610; Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 13610

LENGTH: 342

TYPE: PRP

ORGANISM: Streptomyces avermitilis

US-10-156-761-13610

Query Match 12.9%; Score 294; DB 15; Length 342;
Best Local Similarity 26.5%; Pred. No. 4e-21;
Matches 101; Conservative 66; Mismatches 140; Indels 74; Gaps 17;

QY 34 KVALITAGGLAPCLNSAIGSLIERTEIDPSIBICRGYKGLLDDSPVTAVERKA 93
DB 2 KVALITAGGLAPCLNSAIGSLIERTEIDPSIBICRGYKGLLDDSPVTAVERKA 58
QY 94 GVLORFGGSVIGNSRVKLTNVKDCVKGGLVEGEDPOKVAADOLVKQVDLHTTGDDT 153
DB 59 GILPR--GGTILGSSRTMLMKIEGVER-----VCDNMAALGV 105
QY 154 NTAAADLAFLARNNGYGLTVIGLPRYDNDVPPIKOSIGANTAAEGARF--NNVVAEN 211
DB 106 LGVAAARLT-----DEYGVPAVGVPEKTINDLNDATDYFPGDTAVNATE 160
QY 212 NANPRMLIVHVRNGCMGLTAAATQOEYRKLLDRAEMLPELGLTRESEYEVAAVFPPEAI 271
DB 161 HMR---VLCEVWGRHAGMLAHS-----GLAGGA---NVLLTPEQRF 197
QY 272 DLEAEARLEAVMDKVCUNIFVSGAGVEALVAMQAKQGVPR-----DAFGIKIDAV 327
DB 198 DVDVCAVYTSRFRASVAPIVVAEGA-----MKDQOMVKDLSLSPGVRISGV 249
QY 328 NPGKMGFQEQACMIGAS--KTLVQSGYFAPASASNVDDMLIKSCADLAVECAFRESGV 386
DB 250 --GEMLAKEIEKRGKRAKTTV--LGHVQGGTSPASDRVLTATFGALHAIEAV-----296
QY 387 IGHEDNGNV--LRAIEPPI 405
DB 299 --RDGDFGKVALRGTETIVRV 317

RESULT 9

US-10-156-761-14652

Sequence 14652; Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:

```

APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO: 14652
LENGTH: 341
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-14652

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Query Match 12.5%; Score 284.5; DB 15; Length 341;
Best Local Similarity 27.5%; Pred. No. 3.7e-20;
Matches 97; Conservative 62; Mismatches 143; Indels 51; Gaps 11;

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QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRYGGYKGLLDGSPVTAERVKKA 93
DB 2 RIGVLFGSGDCCGLNNAIVRSVVR-AVVDHDEVIYGFDDGKGLLECY-LKLDLAVS 58
QY 94 GVLORFGGSVIGNSRVKLTNVKDCVKGKLVKGEEDPQKVAADQVNDGVDILHTIGDDT 153
DB 59 GILAR-GGITLSSRVRQPAHLDGVER-----ANGHVAEGLDAIIPIGEGT 105
QY 154 NTAADLAFLAFLANNYGLTVIGLPTVNDVFPKISGAMTAEOGARFYMVAENNA 213
DB 106 LKAARLL-----SDAGLPVGVPKTIINDISATDPTFGFTAVGATAMDLKTTAAS 159
QY 214 NPMILVHEVMGNOCGLMTATAGBYRKLDRAMELPELGITRESYEVNAFVPEALDL 273
DB 160 HORVTLIV-EVMGRHTGMALHSGM-----AAGAHAIIVPERFDDI 198
QY 274 EAEKRLREVMDCVNIPI-SSAGVGAIVAEQAKQGEVPRDAPFGHIXLDVAVN 332
DB 199 EELAKVGERPEAKRRFAIVAAAGAPFRAGSMDF--DEGKADVYGERFAGI--ARQ 252
QY 333 FGEQAFQAGMIGAEKTLVQKSGYFAPASASNVDMRLIKSCADLAVECAFRRESG 385
DB 253 LSLLEERLGEAKRPV-ILGHVQGGTPTATVDRVLATRFGMHAAVEAHRGEGF 304

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RESULT 10
US-10-156-761-10359
Sequence 10359, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10359

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LENGTH: 341
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-10359

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```

Query Match 11.8%; Score 269.5; DB 15; Length 341;
Best Local Similarity 26.8%; Pred. No. 1.2e-18;
Matches 96; Conservative 59; Mismatches 142; Indels 61; Gaps 15;

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QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRYGGYKGLLDGSPVTAERVKKA 93
DB 2 RIGVLFGSGDCCGLNNAIVRSVVRATMYGD-EVIGFEDGYAGLL-DGRYALDLNAVS 58
QY 94 GVLORFGGSVIGNSRVKLTNVKDCVKGKLVKGEEDPQKVAADQVNDGVDILHTIGDDT 153
DB 59 GILAR-GGITLSSRVRQPAHLDGVER-----AQMAREGIDALLPIGEGT 105
QY 154 NTAADLAFLAFLANNYGLTVIGLPTVNDVFPKISGAMTAEOGARFYMVAENNA 213
DB 106 LTAARLL-----SDAGLPVGVPKTIINDISATDPTFGFTAVGATAMDLKTTAAS 159
QY 214 NPMILVHEVMGNOCGLMTATAGBYRKLDRAMELPELGITRESYEVNAFVPEALDL 273
DB 160 HORVTLIV-EVMGRHTGMALHSGM-----ESGVAAGA--HGICLPERFDDP 198
QY 274 EAEKRLREVMDCVNIPI-SSAGVGAIVAEQAKQGEVPRDAPFGHIXLDVAVN 328
DB 199 AHLVYVERFPAKGFAYLC-----VAEGA--HPVGSNDYSIGAL--DQFGERPFGI- 249
QY 329 PGKMFGEQAFQAGMIGAB-KTLVQKSGYFAPASASNVDMRLIKSCADLAVECAFRRESG 385
DB 250 -GTALAALEHRLGEAKRPV--LGHIQGGTPTATVDRVLATRFGMHAAVEAHRGEGF 304

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```

RESULT 11
US-10-369-493-19261
Sequence 19261, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19261
LENGTH: 345
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-10-369-493-19261

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Query Match 11.4%; Score 261; DB 12; Length 345;
Best Local Similarity 26.0%; Pred. No. 9.3e-18;
Matches 96; Conservative 66; Mismatches 141; Indels 66; Gaps 16;

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QY 34 KVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRYGGYKGLLDGSPVTAERVKKA 93
DB 2 KVAVLFGSGDCCGLNNAIVRAVVRANA--HGFEMGLRQGMKGLLEDNHFRLTRET--TS 57
QY 94 GVLORFGGSVIGNSRVKLTNVKDCVKGKLVKGEEDPQKVAADQVNDGVDILHTIGDDT 150
DB 58 GILAR-GGITLSSRVRQPAHLDGVER-----IENGHVAIYAIIG 101
QY 151 DDTNTAADLAFLAFLANNYGLTVIGLPTVNDVFPKISGAMTAEOGARFYMVAENNA 208
DB 102 EGTLSAATRM-----SOGELRIVGVPKTIINDINATDPTFGFTAVGATAMDLKTTAAS 155

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QY 209 AENNANPRLIYHEWNGRNGWLTAAATAGYERKLDRAEMWLELGLTSEYEVHAAVPE 268
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 156 AASH---KRVIVCEVWGRHVMIAI-----YAGIAGAD-----VILVPE 192
QY 269 MAIDLEAEKRL--REVMDKVCVNIIVSEGGAGVEAIVAEOMAKGQVEPRDAFGIKIDA 326
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 193 IPADIAKVAEHIQRRAAGRTPSI--VVAEGTRIKLSADQEQSLVTSGLADENGRPLGG 251
QY 327 VNPGRWFGEFOAQMLGAETLVOKSGYEFAPASASVNDKRL-----IKSCADLAVECAFR 381
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 252 V--GTLIAHEIERRRTGFE--TRSVVGHIGRGAPTRAHDRVLAIRYGVAC--DMVARGEEG 307
QY 382 RESGVIGHD 390
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 KMAALRGND 316

RESULT 12
US-10-369-493-2905
; Sequence 2905, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; LENGTH: 319
; TYPE: PRP
; ORGANISM: Thermotoga maritima
US-10-369-493-2905

Query Match 11.1%; Score 253; DB 12; Length 319;
Best Local Similarity 26.6%; Pred. No. 5,4e-17;
Matches 95; Conservative 60; Mismatches 126; Indels 76; Gaps 14;

QY 33 KVALITAGAGLAPCLNSAIGLIERYTEIDPSIHLICRYGKGLLLGDSYPTAEVRKA 92
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 KXIAVLTSGSDAPGMMAAVRAV-RY-GVROGLEVIYVRRGYSGLIDDF--VKLEYKDV 57
QY 93 AGVLORFGGSVIGNSRVKLTNVKDCVKGGLVEGEDPQKVAADQLVKDGVDLITIGDD 152
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 56 AGITER--GGTILIRCEBEFT-----SEGRILAKQIKKIGISBLVVIIGEG 104
QY 153 TWTAAADLAFLAKNNYGLTVIGLPTVNDVFPPIKOSIGANTAAEGARFMYVAANN 212
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 105 SLT-----GAHLIYEHKLPVVGIPATIDNDIGLIDWCIGVDTCLANTWDAVOKIDTAS 159
QY 213 ANPRMLIYHEWNGRNGWLTAAATAGYERKLDRAEMWLELGLTSEYEVHAAVPEMAID 272
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 160 SHERAFIV--EWMGRHSQYIALMAG-----LYGAE-----AIIVEIIVD 198
QY 273 LEAEAKRELV--MDKVCVNIIVSEGGAGVEAIVAEOMAKGQVEPRDAFGIKIDAVNG 330
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 199 VSQLDRIIEERRRGKINSI--IIVAGASATYVAR-----HDE----- 236
QY 331 KMGFGQFAGMIGAKETLVOKSGYEFAPASASVNDKRLIKSCADLAVECAFRESGVI 387
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 -----YRIGYE--TRITITLHVORGSFTAFDRILALSMGEVAVDALDGSVDVM 284

RESULT 13
US-10-369-493-9669

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; Sequence 9669, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; LENGTH: 357
; TYPE: PRP
; ORGANISM: Desulfitobacterium hafnense
US-10-369-493-9669

Query Match 11.0%; Score 250.5; DB 12; Length 357;
Best Local Similarity 27.4%; Pred. No. 1.1e-16;
Matches 101; Conservative 63; Mismatches 136; Indels 69; Gaps 17;

QY 34 KVALITAGAGLAPCLNSAIGLIERYTEIDPSIHLICRYGKGLLLGDSYPTAEVRKA 93
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 KVALITAGAGLAPCLNSAIGLIERYTEIDPSIHLICRYGKGLLLGDSYPTAEVRKA 93
QY 94 GVLORFGGSVIG-----NSRVKLTNVKDCVKGGLVEGEDPQKVAADQLVKDGVDLIT 148
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 GLIHR--GGTILGTNNRNPFAVPTQV-----GERRQVORSAEVLIRFNAEGIDALIAI 109
QY 149 GGDPTTAADLAFLAKNNYGLTVIGLPTVNDVFPPIKOSIGANTAAEGARFMYVAANN 206
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 GGDPTSLIAEFA-----KQGLKRVGVPTINDLCTDLTRGFQAVAVTAQDALDLH 163
QY 207 VVAENNANPRLIYHEWNGRNGWLTAAATAGYERKLDRAEMWLELGLTSEYEVHAAV 266
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 164 TTAESH--HRIMLESYGRAGHIAL-----YAGVAGAD-----VILI 200
QY 267 PEMALDIE--AEAKRLREVMDKVCVNIIVSEGA--GVEAIVAEOMAKGQVEPRDAFGH 321
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 201 PEIYQLESIAEAVORARLKHPSI--IIVAECAKPLGDMVY--ERTMSGRTDP----- 252
QY 322 IKIDAVNPKMGFGQF--QMGAEKTLVOKSGYEFAPASASVNDKRLIKSCADLAVEC 378
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 253 IKLGLT-----GAKLADLEKVTDMETRVTLGHLORGSPIAVDVLSTRYVAAVEA 306
QY 379 AFRRESGVI 387
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 ALAGDPGM 315

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RESULT 14
US-10-369-493-21998
; Sequence 21998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374

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SEQ ID NO 21998
 LENGTH: 987
 TYPE: PRT
 ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-21998

Query Match 10.8%; Score 246.5; DB 12; Length 987;
 Best Local Similarity 23.9%; Pred. No. 14e-15;
 Matches 103; Conservative 68; Mismatches 135; Indels 125; Gaps 19;

31 KPKKVALITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRYGGYKGLLDSDYPVTAVER 90
 204 KKKKIAVMTSGDPSGMAAVAYVR--TGHEGCVFAVYEGYEGILLRGKRY-----LK 256
 91 KKA-----GVLORGGSVIGSRVYKLTNVKDCVKGGLVKEGDEPOKYAADQVYKGVYDIL 145
 257 KMMEDVKGWLSR--GGTILGTA-----RSMFEFRKRGRRQAGNLISOGIDAL 303
 146 HTGGDDTNTAAADL-----AFLARNY-----GLTVGLPKTVNDVFP 187
 304 VCGGDSGLT--GADLFHEWPSLVDELVAEGRFKEVAYKULSTVGLVGSIDNDMSGT 362
 188 KOSIGAVTAABOGARYTMVAVENNANPRLIVHEWGRNCGMLT---ATAOERYKXL 243
 363 DSTIGAYSALERTCEWVDYIDATKSHRAFYV--EVMGRGCGWLAMAGIATGADY---- 417
 244 DRAEWLELGLTRESYVHAVFVPEMAIDLEAKRLREVMKVDYDCV---NIFVSEGA 298
 418 -----TFPERAVPHGKMODELKEVCQSHRSKGRNNNTIIVABGA 457
 299 -----GYEATVAKQKQOEVRDPAFGHKL--DAVNPGRFGEOFAQMLGAER 345
 458 LDQQLNFTANDVMDALIEL--GLDTKVTILGHVQGGTAVAHNRLLA--LQGVDAVA 512
 346 TLVQKSGYFPAASN-----VDNRKLKSCADLAVBCAFRRBSGVIGHDE 381
 513 AVLS-----FTPEPSPPLIGILENKIIRMLVESVKLTQSYA-----TAINKOF 557
 392 DNGNVLNIAEF 402
 558 DKXISLRDTER 568

RESULT 15
 US-09-815-242-13785
 Sequence 13785; Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselebeck, Robert
 APPLICANT: Ohlson, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 13785
 LENGTH: 320
 TYPE: PRT
 ORGANISM: Salmonella typhi
 US-09-815-242-13785

Query Match 10.5%; Score 240.5; DB 9; Length 320;
 Best Local Similarity 24.8%; Pred. No. 1e-15;
 Matches 102; Conservative 59; Mismatches 122; Indels 129; Gaps 18;

33 KKVAILITAGGLAPCLNSAIGSLIERYTEIDPSIEIICRYGGYKGL-----LLDSYPVTA 87
 3 KKGIVITSGGDAFGMAAIRGVVR--AALTEGLFVWGIYDYLGLYEDRWVQIDRYSVSD 60
 88 EVRKAGVLRPGGSVIGSRVYKLTNVKDCVKGGLVKEGDEPOKYAADQVYKGVYDILFT 147
 61 MNR-----GTFVLSAR--FPEFRD-----ENIRAVALEMLKTRGIDALV 100
 148 IGGDDTNTAAADLAAFLANNYGLTVTGLPKTVNDVFPKOSLGAMTAABOGARYFMV 207
 101 IGGDGSYMGAKEL-----TEWGPICIGLPTIIDNDKGTDTIGFTALGVVEAIDRL 154
 208 VABNNANPRLIVHEWGRNCGMLTNATQERYKLDRAEML--BELGLTRESYVHAVF 265
 155 RUTSSHQHISIV--EVMGRYCGDLTLAA-----TAGGCEFTVVEVEFNR----- 200
 266 VPEMAIDLEAK-----RLREVMKVDVCFNIFVSEGAVE--AIVAKQAK 310
 201 -----DLVATIKAGIAKAKKRAIYALITHMCDVBLAFIERKGRFETRAVTLGHIOG 254
 311 GQSVPRDPAFGHKLDAVNPGRFGEOFAQMLGAERTLVQKSGYFPAASNVDNMLIKS 370
 255 GSPVPYD-----RILASRMAYV----- 272
 371 CADLAVE-----CAPRRBSGVIGHDEDNQNVRLAIEFPRINKGKRPNIDTW 417
 273 -IDLILBHGRCVGIQNEQVLVHD-----ITDAIENRK--RPFK--SDW 312

Search completed: January 29, 2004, 14:43:34
 Job time : 40 secs